Sequence 16, Sequence 18, Sequence 16,

Sequence 6, Sequence 16, Sequence 18,

Sequence 2,

Run on:

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US-10-225-784-2
US-10-225-784-6
US-09-564-329A-16
US-09-564-329A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-855-153-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-09-934-586A-2
   RESULT
                                                                                                     August 18, 2003, 19:56:50 ; Search time 55 Seconds (without alignments) 292.971 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                               US-09-934-586A-2
123
1 MKAVLLALLMAGLALQPGTA......AAILALLPALGLLLWGPGQL 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. / cgn2_6/ptodata1/lpubpaa/USO7 PUBCOMB.pep:*
2. / cgn2_6/ptodata1/lpubpaa/USO7 PUBCOMB.pep:*
3. / cgn2_6/ptodata1/lpubpaa/USO6 PUBCOMB.pep:*
3. / cgn2_6/ptodata1/lpubpaa/USO6 PUBCOMB.pep:*
5. / cgn2_6/ptodata1/lpubpaa/USO6 PUBCOMB.pep:*
6. / cgn2_6/ptodata1/lpubpaa/USO8_PUBCOMB.pep:*
7. / cgn2_6/ptodata1/lpubpaa/USO8_PUBCOMB.pep:*
8. / cgn2_6/ptodata1/lpubpaa/USO8_PUBCOMB.pep:*
9. / cgn2_6/ptodata1/lpubpaa/USO8_PUBCOMB.pep:*
10. / cgn2_6/ptodata1/lpubpaa/USO8_PUBCOMB.pep:*
11. / cgn2_6/ptodata1/lpubpaa/USO8_PUBCOMB.pep:*
12. / cgn2_6/ptodata1/lpubpaa/USO8_PUBCOMB.pep:*
13. / cgn2_6/ptodata1/lpubpaa/USO8_PUBCOMB.pep:*
14. / cgn2_6/ptodata1/lpubpaa/USIOA_PUBCOMB.pep:*
15. / cgn2_6/ptodata1/lpubpaa/USIOA_PUBCOMB.pep:*
16. / cgn2_6/ptodata1/lpubpaa/USIOA_PUBCOMB.pep:*
17. / cgn2_6/ptodata1/lpubpaa/USIOA_PUBCOMB.pep:*
18. / cgn2_6/ptodata1/lpubpaa/USIOA_PUBCOMB.pep:*
19. / cgn2_6/ptodata1/lpubpaa/USIOA_PUBCOMB.pep:*
11. / cgn2_6/ptodata1/lpubpaa/USIOA_PUBCOMB.pep:*
12. / cgn2_6/ptodata1/lpubpaa/USIOA_PUBCOMB.pep:*
13. / cgn2_6/ptodata1/lpubpaa/USIOA_PUBCOMB.pep:*
14. / cgn2_6/ptodata1/lpubpaa/USIOA_PUBCOMB.pep:*
15. / cgn2_6/ptodata1/lpubpaa/USIOA_PUBCOMB.pep:*
16. / cgn2_6/ptodata1/lpubpaa/USIOA_PUBCOMB.pep:*
17. / cgn2_6/ptodata1/lpubpaa/USIOA_PUBCOMB.pep:*
18. / cgn2_6/ptodata1/lpubpaa/USIOA_PUBCOMB.pep:*
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                GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Total number of hits satisfying chosen parameters:
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US-09-564-329A-6
US-09-854-329A-6
US-09-855-153-6
US-09-855-153-6
US-09-854-811-2
US-09-934-773-6
US-09-934-773-6
US-09-934-773-6
US-09-93-63-620-2
US-09-963-620-2
                                                                                                                                                                                                                                                                            492763 segs, 131003257 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published Applications_AA:
                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Listing first 45 summaries
                                                                         OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Match Length DB
                              Copyright
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                                                                                                                                                                  Title:
Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                           Word size
                                                                                                                                                                                                                                                                            Searched:
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Sequence 17,

Sequence 4, Sequence 7,

Sequence 17

Sequence 1' Sequence 1

Sequence

Sequence 4, Sequence 7,

Sequence 17, Sequence 17, Sequence 17,

Sequence

Sequence 1 Sequence 1 Sequence 1

Sequence

Sequence

Sequence Sequence

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Sequence 2, Application US/09934586A
Patent No. US20020058241A1
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                         ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
FILING DATE: 23-Aug-2001
PRIOR APPLICATION NUMBER: US/09/934,586A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 96,749
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 09/225,080
FILING DATE: «Unknown:
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
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Appli Appli Appli Appli Appli

Sequence

Result è Sequence 6, Sequence 2, Sequence 6, Sequence 2, Sequence 6, Sequence 6, Sequence 6,

Sequence 2, Sequence 6,

US-09-855-632-6 US-10-224-720-2 US-10-224-720-6

Sequence 2 Sequence 6

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US-09-564-329A-6
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US-09-855-153-2
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APPLICANT: Witte, Owen N.

APPLICANT: Witte, Owen N.

APPLICANT: Witte, Owen N.

TITLE OF INVENTION: SAfferan, DOUGIAS C.

TITLE OF INVENTION: PECA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF FILE REFERENCE: 30435.540S14

CURRENT APPLICATION NUMBER: US/09/564,329A

CURRENT PILING DATE: 1999-07-20

PRIOR APPLICATION NUMBER: 09/314,279

PRIOR PELING DATE: 1999-07-10

PRIOR PELING DATE: 1998-01-12

PRIOR APPLICATION NUMBER: 60/074,675

PRIOR APPLICATION NUMBER: 60/113,230

PRIOR FILING DATE: 1998-02-17

PRIOR FILING DATE: 1999-02-17

PRIOR FILING DATE: 1999-03-16

PRIOR FILING DATE: 1999-02-17

PRIOR FILING DATE: 1999-03-10

PRIOR FILING DATE: 1999-03-10

PRIOR FILING DATE: 1999-02-17

PRIOR FILING DATE: 1999-03-10

PRIOR FILING DATE: 1999-03-10
                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                           Length 123;
                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                              99.2%; Score 122; DB 9;
100.0%; Pred. No. 8e-104;
ive 0; Mismatches 0;
                                                                                                                    CLONE: <Unknown>
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09564329A
Patent No. US20010055751A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: HUMAN PSCA (hPSCA)
                             MOLECULE TYPE: peptide
IMMEDIATE SOURCE: 1
LIBRARY: SCAH-2
TOPOLOGY: linear
                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 123; Conservative
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US-09-564-329A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INCREMATION:

APPLICANT: Reiter, Robert E.

APPLICANT: Witte, Owen N.

APPLICANT: Witte, Owen N.

TITLE OF INVENTION: PECA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

FILE REFERENCE: 30435.540S1

CURRENT APPLICATION NUMBER: US/09/564,329A

CURRENT PELLING DATE: 1999-07-20

PRIOR APPLICATION NUMBER: 09/315,326

PRIOR FILING DATE: 1998-07-30

PRIOR FILING DATE: 1998-07-30

PRIOR FILING DATE: 1998-01-12

PRIOR PELLORICATION NUMBER: 60/071,141

PRIOR PLILING DATE: 1998-02-17

PRIOR PLILING DATE: 1998-12-21

PRIOR FILING DATE: 1998-12-21

PRIOR FILING DATE: 1998-12-21

PRIOR FILING DATE: 1999-02-17

PRIOR FILING DATE: 1999-03-16

PRIOR FILING DATE: 1999-03-16

PRIOR FILING DATE: 1999-03-16

PRIOR FILING DATE: 1999-03-16

PRIOR FILING DATE: 1999-02-17

PRIOR FILING DATE: 1999-05-25

NUMBER OF SEQ ID NOS: 27
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Length 123;
    DB 9; Le
2.3e-77;
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Query Match 75.6%; Score 93; DB Best Local Similarity 100.0%; Pred. No. 2.3 Matches 93; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/09564329A Patent No. US20010055751A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09855153 patent No. US20020102666A1
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ORGANISM: HUMAN PSCA (hPSCA)
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1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLT 60
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Sequence 2, Application US/09854811

GENERAL INPORMATION:

APPLICANT: Witter, Owen N.

APPLICANT: Witter, Owen N.

APPLICANT: Saffarm, Douglas C.

TITLE OF INVENION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

FILE REPERENCE: 30435.54US14

CURRENT APPLICATION NUMBER: US/09/854,811

CURRENT APPLICATION NUMBER: 09/554,811

CURRENT FILING DATE: 2001-05-14

PRIOR FILING DATE: 2000-05-03

PRIOR FILING DATE: 1999-07-20

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PALENTIN VET: 2.0

SEQ ID NO 2

LENGTH: 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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2.3e-77;
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100.0%; Pred. No. ...
0; Mismatches
          PRIOR APPLICATION NUMBER: 08/814,279
PRIOR FILING DATE: 1997-03-10
PRIOR FILING DATE: 1998-01-12
PRIOR FILING DATE: 1998-01-12
PRIOR PILING DATE: 1998-01-12
PRIOR PILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-12-21
PRIOR PILING DATE: 1999-02-17
PRIOR PILING DATE: 1999-03-16
PRIOR PILING DATE: 1999-03-16
PRIOR PLING DATE: 1999-03-16
PRIOR PILING DATE: 1999-03-16
PRIOR PILING DATE: 1999-03-16
PRIOR PILING DATE: 1999-03-16
PRIOR PILING DATE: 1998-03-16
PRIOR PILING DATE: 1998-02-17
PRIOR FILING DATE: 1998-02-17
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATCHTIN VEY: 2.0
SEQ ID NO 6
FUNDATION OF 2.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: HUMAN PSCA (hPSCA)
US-09-855-153-6
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Best Local Similarity 100.0
Matches 93; Conservative
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APPLICANT: MITCH OWGEN N.
APPLICANT: MITCH OWGEN N.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILER REPERENCE: 30435-541814
FILER REPERENCE: 30435-541814
CURRENT APPLICATION NUMBER: 09/564,329
FRIOR FILLING DATE: 2000-05-03
FRIOR APPLICATION NUMBER: 09/559,326
FRIOR FILLING DATE: 1999-07-20
FRIOR APPLICATION NUMBER: 09/359,326
FRIOR FILLING DATE: 1999-07-30
FRIOR PELLING DATE: 1999-07-30
FRIOR PELLING DATE: 1999-07-10
FRIOR PELLING DATE: 1999-01-12
FRIOR PELLING DATE: 1999-02-13
FRIOR FILLING DATE: 1998-02-13
FRIOR FILLING DATE: 1999-02-17
FRIOR FILLING DATE: 1999-02-17
FRIOR PELLING DATE: 1999-03-16
FRIOR FILLING DATE: 1999-03-16
FRIOR FILLING DATE: 1999-03-16
FRIOR FILLING DATE: 1999-03-16
FRIOR FILLING DATE: 1999-03-10
FRIOR FILLING DATE: 1999-02-17
FRIOR FILLING DATE: 1999-03-10
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APPLICANT: Witte, Owen N.
APPLICANT: Witte, Owen N.
APPLICANT: Witte, Owen N.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF FILE REFERENCE: 30435.54US14
CURRENT APPLICATION UNMBER: US/09/855,153
CURRENT FILLING DATE: 2001-16-14
PRIOR APPLICATION NUMBER: 09/564,329
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Patent No. US20020102666Al
GENERAL INFORMATION:
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FEATURE:
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SITE
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7: SITE
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FILING DATE: 1998-02-13
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                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/09854811

Parent No. US20020119157A1

GENERAL INFORMATION:

APPLICANT: Reiter. Robert E.

APPLICANT: Mitte, Owen N.

APPLICANT: Saffran, Douglas C.

TITLE OF INVENTION: PRCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

FILE REFERENCE: 30435.54US14

CURRENT FILING DATE: 2001-05-14

CURRENT FILING DATE: 2000-05-14

PRIOR FILING DATE: 2000-05-03

PRIOR FILING DATE: 1099-07-20

NUMBER OF SEQ ID NOS: 27

SOUTHARE: PALCHING UNCE: 2.00
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Fatent No. US20020136689A1

GENERAL INFORMATION:

APPLICANT: Reiter, Robert E.

APPLICANT: Witte, Owen N.

APPLICANT: Witte, Owen N.

APPLICANT: Saffran, Douglas C.

TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

FILE REFERENCE: 30435.54US14

CURRENT APPLICATION NUMBER: US/09/934,773

CURRENT FILING DATE: 2000-08-21

FRIOR FILING DATE: 2000-05-03

PRIOR FILING DATE: 1999-07-20

PRIOR APPLICATION NUMBER: 09/814,279

PRIOR FILING DATE: 1999-07-20

PRIOR FILING DATE: 1999-07-31

PRIOR FILING DATE: 1999-07-31

PRIOR FILING DATE: 1999-07-31

PRIOR FILING DATE: 1999-07-31

PRIOR APPLICATION NUMBER: 60/071,141

PRIOR APPLICATION NUMBER: 60/071,141
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                                              Length 123;
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                                                                                     0; Indels
                                         Score 93; DB 10; I
Pred. No. 2.3e-77;
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                           75.6%; Scc...
100.0%; Pred. No. ...
0; Mismatches
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, ORGANISM: HUMAN PSCA (hPSCA)
US-09-854-811-6
                                         Query Match 75.6
Best Local Similarity 100.
Matches 93; Conservative
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US-09-934-773-2
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US-09-854-811-2
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APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Owen N.
APPLICANT: Witte, Owen N.
APPLICANT: Witte, Owen N.
APPLICANT: Safferan, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.540S14
CURRENT APPLICATION NUMBER: US/09/934,773
CURRENT FILING DATE: 2000-08-21
PRIOR PRICATION NUMBER: 09/359,326
PRIOR FILING DATE: 1999-07-20
PRIOR PELICATION NUMBER: 08/814,279
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1998-01-12
PRIOR FILING DATE: 1998-01-12
PRIOR FILING DATE: 1998-01-12
PRIOR FILING DATE: 1998-01-23
PRIOR FILING DATE: 1998-12-21
PRIOR FILING DATE: 1998-02-33
PRIOR FILING DATE: 1998-02-33
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-17
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Best Local Similarity 100.0%; Pred. No. 2.3e-77;
Matches 93; Conservative 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: 60/113,230
PRIOR FILING DATE: 1998-12-21
PRIOR FILING DATE: 1998-12-21
PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 60/120,536
PRIOR APPLICATION NUMBER: 60/124,658
PRIOR APPLICATION NUMBER: 60/038,261
PRIOR FILING DATE: 1999-03-10
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-12-02
PRIOR PILING DATE: 1999-10-17
PRIOR PILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 09/251,835
PRIOR APPLICATION NUMBER: 09/251,835
PRIOR PILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PALENTIN VEY: 2.0
SEQ ID NO 2
LENGTH: 123
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PRIOR APPLICATION NUMBER: 09/038,261
PRIOR FILING DATE: 1998-03-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: HUMAN PSCA (hPSCA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .. (64)
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NAME/KEY: SITE
LOCATION: (67)..(81)
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LOCATION: (50).
NAME/KEY: SITE
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1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLT.60
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APPLICANT: Mite, Owen N.
APPLICANT: Mite, Owen N.
APPLICANT: Mite, Owen N.
APPLICANT: Mite, Owen N.
TITLE OF INVENTION: PSCA: PROGTATE STEM CELL ANTIGEN AND USES THEREOF
FILE OF INVENTION: PSCA: PROGTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435,540S14
CURRENT FILING DATE: 2004-09-26
PRIOR APPLICATION NUMBER: 09/564,329
PRIOR APPLICATION NUMBER: 09/564,329
PRIOR APPLICATION NUMBER: 06/074,675
PRIOR APPLICATION NUMBER: 60/074,675
PRIOR APPLICATION NUMBER: 60/074,675
PRIOR APPLICATION NUMBER: 60/113,230
PRIOR APPLICATION NUMBER: 60/113,230
PRIOR APPLICATION NUMBER: 60/113,230
PRIOR APPLICATION NUMBER: 60/124,658
PRIOR APPLICATION NUMBER: 60/124,658
PRIOR APPLICATION NUMBER: 60/124,658
PRIOR PELING DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-17
PRIOR PELING DATE: 1999-03-17
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75.6%; Score 93; DB 10; 1
Best Local Similarity 100.0%; Pred. No. 2.3e-77;
Matches 93; Conservative 0; Mismatches 0;
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75.6%; Score 93; DB 10;
Best Local Similarity 100.0%; Pred. No. 2.3e-77;
Matches 93; Conservative 0; Mismatches 0;
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; ORGANISM: HUMAN PSCA (hPSCA)
US-09-963-620-6
       ; LOCATION: (71)..(82)
; NAME/KEY: SITE
; LOCATION: (67)..(81)
US-09-963-620-2
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Sequence 2, Application US/09963620

Sequence 2, Application US/09963620

Sequence 2, Application US/09963620

Septiment No. US20020141941A1

APPLICANT: Witte, Owen N.

APPLICANT: Saffran, Dowel N.

APPLICANT: Saffran, Dowel N.

APPLICANT: Saffran, Dowel N.

CURRENT FILING DATE: 2001-09-26

FRIOR FILING DATE: 2001-09-26

FRIOR PELICATION NUMBER: 09/564,329

FRIOR FILING DATE: 1999-02-03

FRIOR PELICATION NUMBER: 09/14,279

FRIOR PELICATION NUMBER: 09/14,279

FRIOR PELICATION NUMBER: 09/071,141

FRIOR PELICATION NUMBER: 06/071,141

FRIOR FILING DATE: 1999-01-12

FRIOR FILING DATE: 1999-01-13

FRIOR PELICATION NUMBER: 60/113,230

FRIOR FILING DATE: 1999-02-13

FRIOR APPLICATION NUMBER: 60/120,536

FRIOR PELICATION NUMBER: 60/120,536

FRIOR FILING DATE: 1999-03-10

FRIOR FILING DATE: 1999-05-17

FRIOR FILING DATE: 1999-05-17
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PRIOR APPLICATION NUMBER: 09/203,939
PRIOR PILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: 09/251,835
PRIOR FILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 6
LENGTH: 123
                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: HUMAN PSCA (hPSCA)
US-09-934-773-6
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LOCATION: (50)..(64)
NAME/KEY: SITE
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                                                                                               APPLICANT: Wite, Owen N
APPLICANT: Wite, Owen N
APPLICANT: Wite, Owen N
APPLICANT: Wite, Owen N
APPLICANT: SETERA, DOUGLAB C.
ITILE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
ITILE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
ITILE REFERENCE: 30435.540514
CURRENT FILING DATE: 2001-05-14
FRIOR APPLICATION NUMBER: 09/359,326
FRIOR APPLICATION NUMBER: 09/359,326
FRIOR APPLICATION NUMBER: 09/359,326
FRIOR APPLICATION NUMBER: 06/071,141
FRIOR FILING DATE: 1999-07-20
FRIOR APPLICATION NUMBER: 60/071,141
FRIOR FILING DATE: 1998-07-21
FRIOR FILING DATE: 1998-02-13
FRIOR FILING DATE: 1999-02-13
FRIOR APPLICATION NUMBER: 60/113,230
FRIOR FILING DATE: 1999-02-13
FRIOR FILING DATE: 1999-02-10
FRIOR PLING DATE: 1999-02-10
FRIOR FILING DATE: 1999-03-10
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100.0%; Pred. No. 2.3e-77;
tive 0; Mismatches 0; Indels
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Sequence 2, Application US/09855632
Publication No. US20030113818A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: HUMAN PSCA (hPSCA)
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Best Local Similarity
Matches 93; Conserval
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; LOCATION: (67)..(81)
US-09-855-632-2
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Sequence 6, Application US/0985532
Publication No. US20030113818A1
GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Owen N.

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NUMBER OF SEQ ID NOS: 27
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| US-10-24-7.0-6
| US-10-24-7.0-6
| US-20-24-7.0-6
| US-20030147806A1
| GENERAL INFORMATION:
| APPLICANT: Reiter, Robert E. |
| APPLICANT: Reiter, Owen N. |
| APPLICANT: Safferan, Douglas C. |
| TITLE OF INVENTION: BACKA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF FILE REFERENCE: 30435.540S14 |
| CURRENT PAPLICATION NUMBER: US/09/359,326 |
| PRIOR FILING DATE: 1999-07-20 |
| PRIOR APPLICATION NUMBER: 06/071,141 |
| PRIOR FILING DATE: 1997-03-10 |
| PRIOR FILING DATE: 1998-01-12 |
| PRIOR PILING DATE: 1998-01-12 |
| PRIOR PILING DATE: 1998-01-12 |
| PRIOR PILING DATE: 1998-01-12 |
| PRIOR FILING DATE: 1998-01-12 |
| PRIOR APPLICATION NUMBER: 60/113,230 |
| PRIOR FILING DATE: 1999-02-17 |
| PRIOR FILING DATE: 1999-02-17 |
| PRIOR FILING DATE: 1999-02-17 |
| PRIOR FILING DATE: 1999-03-16 |
| PRIOR FILING DATE: 1999-03-16 |
| PRIOR FILING DATE: 1998-03-16 |
| PRIOR FILING DATE: 1998-03-16 |
| PRIOR FILING DATE: 1998-03-10 |
| PRIOR FILING DATE: 1999-03-10 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.6%; Score 93; DB 12; Length 123; 100.0%; Pred. No. 2.3e-77; ive 0; Mismatches 0; Indels
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PRIOR FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 60/124,658
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1998-03-10
PRIOR FILING DATE: 1998-12-02
PRIOR PILING DATE: 1998-12-02
PRIOR APPLICATION NUMBER: 09/251,835
PRIOR PILING DATE: 1999-02-17
Remaining Prior Application data removed - S; NUMBER OF SEC ID NOS: 2.0
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: HUMAN PSCA (hPSCA)
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Matches 93; Conservative
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LOCATION: (50)..(64)
FEATURE:
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LOCATION: (71)..(82)
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; LOCATION: (67).
US-10-224-720-2
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 18, 2003, 19:52:00 ; Search time 40 Seconds (without alignments) 295.719 Million cell updates/sec

US-09-934-586A-2 123 1 MKAVLLALLMAGLALQPGTA......AAILALLPALGLLLWGPGQL 123

Title: Perfect score: Sequence: OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

283308 seqs, 96168682 residues Searched:

0 Word size :

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200g000000

Post-processing: Listing first 45 summaries

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	G protein-coupled	GlnR protein - Str	hypothetical prote			alpha-1A-adrenergi	alpha-1A adrenergi	alpha-1A-adrenergi	trbO protein - Ent	guanine-nucleotide	guanine-nucleotide	hypothetical prote		_			hypothetical prote	signal peptidase I	conserved hypothet	fibroblast growth	hypothetical prote	protein C28H8.4 [i	hypothetical prote	phosphoglycolate p			ycolate	-~	hypothetical 30.3K
	ID	D48909	JN0831	T23158	AF3509	H75060	JH0447	A38731	139369	T08512	\$29714	152427	F82716	T22693	E87507 .	T48784	A95864	F72277	G69707	A75270 '	TVHUHS	T25161	H88469	T30618	S55288	A86003	C91157 .	AH1000	T36243	A97359
	DB	¦ ~	~	~	~	~	~	7	7	~	7	~	~	~	~	~	~	N	~	~	٦	~	~	~	~	~	~	~	7	7
	Length	161	267	284	299	486	501	260	572	88	123	123	123	145	150	166	173	191	193	198	206	206	213	213	252	252	252	252	255	273
æ	Query Match	6.5	6.5	6.5	6.5	6.5	6.5	6.5	6.5	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7
	Score	8	80	ω	œ	œ	œ	80	ω	7	7	7	7	7	7	. 7	7	7	7	7	7	7.	7	7	7	7	7	7	7	7
•	Result No.	-	7	m	4	ß	9	7	80	σ	10	11	12	13	14	15	16	17	18	19		21			24	25	56	27	28	29

conserved hypothet	conserved hypothet	nonstructural prot	sulfate transport	probable ABC trans	hypothetical prote	probable antibioti	hypothetical prote	conserved hypothet	hypothetical prote	hypothetical prote	iron(III) dicitrat	probable ABC-trans	probable hemin deg	probable transamin	conserved hypothet
AB2577	G69766	C48547	AG1846	B95316	A83109	H75439	AH2295	AH3121	G98165	A70664	AB2129	A70849	A83059	B70876	G72306
7	N	~	7	7	~	~	N	N	N	~	~	7	~	~	7
273	287	290	291	291	296	296	303	329	329	345	346	349	354	362	365
5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7
7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7
30	31	32	33	34	35	36	37	38	39	40	11	12	13	44	45

ALIGNMENTS

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RESULT 1
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G protein-coupled receptor Gpcr8 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 0.10-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 19-May-2000
C;Accession: D48909
R;Wilkie, T.M.; Chen, Y.; Gilbert, D.J.; Moore, K.J.; Yu, L.; Simon, M.I.; Copeland, N.G Genomics 18, 175-184, 1993
A;Title: Identification, chromosomal location, and genome organization of mammalian G-prc A;Reference number: A48909; MUID:94116980; PMID:8288218
A;Accession: D48909
A;Accession: D48909
A;Statues: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-161 < WILL>

A;Cross-references: GB:L20333 C;Superfamily: vertebrate rhodopsin C;Keywords: G protein-coupled receptor

Gaps ö Length 161; 0; Indels Query Match 6.5%; Score 8; DB 2; Best Local Similarity 100.0%; Pred. No. 3.5; Matches 8; Conservative 0; Mismatches

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GINR protein - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 19-May-2000

C;Accession: JN0831 R;Wray Jr., L.V.; Fisher, S.H. Gene 130, 145-150, 1993 A;Title: The Streptomyces coelicolor glnR gene encodes a protein similar to other bacter A;Reference number: JN0831; MUID:93345814; PMID:7688332

A,Accession: JN0831
A;Molecule type: DNA
A;Residues: 1-267 <WRA>
A;Residues: 1-267 <WRA>
A;Residues: 1-267 <WRA>
A;Cresnces: GB:L03213; NID:g153282; PIDN:AAA02838.1; PID:g153283
C;Comment: This protein positively regulates the transcription of glutamine synthetase.
C;Comment: This protein is a member of the sub-family of response regulator proteins.

C;Genetics:

A;Gene: glnR C;Superfamily: ompR protein; response regulator homology C;Keywords: DNA binding; phosphoprotein; transcription regulation

Length 267; Query Match 6.5%; Score 8; DB 2; Best Local Similarity 100.0%; Pred. No. 5.2; Matches 8; Conservative 0; Mismatches

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Gaps ö

0; Indels

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A; Gene: CESP: K01A6.4

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110

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C,Accession: JH0447

C,Bricos, O.F.; Whittaker, J.; Song, J.; Berelowitz, M.
Biochem. Biophys. Res. Commun. 179, 1485-1490, 1991

A,Title: Molecular cloning and sequencing of a cDNA encoding a human alpha 1A adrenergic

A,Reference number: JH0447; MUID:92028892; PMID:1656955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alpha-lA adrenergic receptor - rat
Cispecies: Rattus norvegicus (Norway rat)
Cjate: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Apr-2000
CjAccession: A38731; A53220
R;Lomasney, J.W.; Cotecchia, S.; Lorenz, W.; Leung, W.Y.; Schwinn, D.A.; Yang-Feng, T.L.
Biol. Chem. 266, 6365-6369, 1991
A;Title: Molecular cloning and expression of the cDNA for the alpha-lA-adrenergic recept
A;Reference number: A38731; WUID:91177889; PMID:1706716
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
                                                                                                                                                                                                A;Cross-references: GB:AJ248287; GB:AL096836; NID:g5458657; PIDN:CAB50381.1; PID:g545889
A;Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                  C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ1309
C;Reywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alpha-1A-adrenergic receptor - human
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 13-Aug-1999
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A;Residues: 1-560 aLOM>
A;Cross-treferences: GB:M6054; NID:g202761; PIDN:AAA63477.1; PID:g202762
R;Perez, D.M.; Piascik, M.T.; Graham, R.M.
Mol. Pharmacol. 40, 876-883, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #status predicted <TM4>
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F,172-196/Domain: transmembrane #status predicted <TM4>
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100.0%; Pred. No. 8.5;
tive 0; Mismatches
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Pred. No. 8.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            6.5%; (
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Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
                                    A,Description: Pyrococcus & A,Reference number: A75001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 AAAILALL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              457 MKAVLLAL 464
                                                                                                                                                                              A; Residues: 1-486 < KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-501 <BRU>
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                                                                                                                     A;Status: preliminary A;Molecule type: DNA
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                                                                                          A; Accession: H75060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R.Dellecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, F.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
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A;Cross-references: GB:AE008917; PIDN:AAL53241.1; PID:g17984119; GSPDB:GN00190
A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF3509
ATP/GTP-binding protein BMEI2060 [imported] - Brucella melitensis (strain 16M)
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A;Cross-references: EMBL:Z68750; PIDN:CAA92963.1; GSPDB:GN00022; CESP:K01A6.4
A;Experimental source: clone K01A6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
C;Accession: AF3509
                                                                                                                                                                                                   hypothetical protein KO1A6.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C;Accession: T23158
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A;Introns: 89/3; 104/3; 126/3
C;Superfamily: Phaseolus glycine-rich cell wall protein 1.8
                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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100.0%; Pred. No. 5.7;
live 0; Mismatches
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                                                                                                                                                                                                                                                                                                                        R;Cottage, A. Bubmitted to the EMBL Data Library, January 1996 A;Reference number: 219701 A;Reference number: A;Acession: T23158
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C;Superfamily: ydiA protein
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         LPALGLLL 117
                                                               LPALGLLL 25
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Best Local Similarity
Matches 8; Conserva
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A;Status: preliminary A;Molecule type: DNA

A,Gene: BMEI2060

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C;Genetics:

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RiThorsted, P.B.; Shah, D.S.; Macartney, D.; Kostelidou, K.; Thomas, C.M. Plasmid 36, 95-111, 1996
A;Title: Conservation of the genetic switch between replication and transfer genes of In-A;Reference number: Z16434; MUID:97118926; PMID:8954881
A;Accession: T08512
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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R;Yu, H.; Schreiber, S.L.
Biochemistry 34, 9103-9110, 1995
A;Title: Cloning, Zn2+ binding, and structural characterization of the guanine nucleotid A;Reference number: 152427; MUID:95345082; PMID:7619808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Burton, J.; Roberts, D.; Montaldi, M.; Novick, P.; de Camilli, P. Nature 361, 464-467, 1993
A;Title: A mammalian guanine-nucleotide-releasing protein enhances function of yeast A;Reference number: S29714; MUID:93156814; PMID:8429887
                                                                                                                                                                                                                           A;Residues: 1-88 <THO>
A;Cross-references: EMBL:U67194; NID:g1572520; PIDN:AAC64456.1; PID:g1572561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
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C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
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C;Genetics:
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100.0%; Pred. No. 26;
iive 0; Mismatches
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Best Local Similarity 100
Matches 7; Conservative
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Best Local Similarity
7, Conserve
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Best Local Similarity
Matches 7; Conserv
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A,Title: Solution-phase library screening for the identification of rare clones: isolati
A,Reference number: A53280, MUID:92100054, PMID:1661838
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A;Residues: 1.572 <RES>
A;Cross-references: GB:D29952; NID:g914933; PIDN:BAA06222.1; PID:g914934
R;Across-references: GB:D29952; NID:g914933; PIDN:BAA06222.1; PID:g914934
R;Weinberg, D.H.: Trivedi, P.; Tan, C.P.; Mitra, S.; Perkins-Barrow, A.; Borkowski, D.;
Biochem. Biophys. Res. Commun. 201, 1296-1304, 1994
Biochem. Biophys. Res. Commun. 201, 1296-1304, 1994
A;Title: Cloning, expression and characterization of human alpha adrenergic receptors al A;Reference number: JC2331; MUID:94296402; PMID:8024574
A;Accession: JC2331
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R; Esbenshade, T.A.; Hirasawa, A.; Tsujimoto, G.; Tanaka, T.; Yano, J.; Minneman, K.P.; Isbenshade, T.A.; Hirasawa, A.; Tsujimoto, G.; Tanaka, T.; Yano, J.; Minneman, K.P.; Isbenshade, T.A.; Hirasawa, A.; Tsulian alpha 1d-adrenergic receptor and inducible expression of A; Reference number: 139369; MulD:95265059; PMID:7746284
A; Accession: 139369
A; Asterus: preliminary; translated from GB/EMBL/DDBJ
                                                  A; Accession: A53280
A; Status: preliminary: not compared with conceptual translation
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Esiduse: 1-36, Pr. 38-58, I', 60-202, I', 204-305, R', 307-366, I', 368-370, I', 372-559
A; Experimental source: hippocampus
A; Note: sequence extracted from NCBI backbone (NCBIP:73541)
C; Superfamily: vertebrate rhodopsin
C; Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
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C;Species: Enterobacter aerogenes
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
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A;Residues: 1-30,'G',32-521,'P',523-572 <WEI>
A;Note: the authors translated the codon CCC for residue 522 as Arg
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100.0%; Pred. No.
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100.0%; Pred. No.
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Cross-references: GDB:118749; OMIM:104219
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Best Local Similarity 100.
Matches 8; Conservative
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C,Species: Homo sapiens (man)
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A;Residues: 1-572 <R
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Gaps

RESULT 9

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Query Match
Best Local Similarity 100.
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A; Residues: 1-123 «SIM»
A; Cross-references: GB:AE003950; GB:AE003849; NID:g9106104; FIDN:AAF83960.1; GSPDB:GN001
A; Experimental source: strain 9a5c
R; Simpson, A.J. G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. Briones, M.S.; Bueno, M.S.; Ferro, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr Chado, M.A.; Madelira, A.M.B.N.; Matesidera, H.M.F.; Martino, C.L.; Marques, M.Y.; Martins, E.A.; Mandelira, M.R.; Matesidues, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Authors: Asilva, A.C.R.; da Silva, F.R.; da Silva, F.R.; da Silva, F.R.; da Silva, A.C.R.; da Silva, F.N.; Silva Jr., W.A.; da Silvaira, A; Contentes: annotation
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; FILSO
                                                                                                                                                                        hypotherical protein XF1150 [imported] - Xylella fastidiosa (strain 9a5c)
C,Species: Xylella fastidiosa
C,Species: Xylella fastidiosa
C,Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C,Accession: F82710
R,anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen Nature 406, 151-157, 2000
A,Fitle: The genome sequence of the plant pathogen Xylella fastidiosa.
A,Fitle: The genome sequence of the plant pathogen Xylella fastidiosa.
A,Reference number: A82515; MUID:20365717; PMID:10910347
A,Note: for a complete list of authors see reference number A59228 below
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A;Residues: 1-145 <WIL>
A;Cross-references: EMBL:Z83318; PIDN:CAB05900.1; GSPDB:GN00022; CESP:F55B11.4
A;Experimental source: clone F55B11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F55B11.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T22693
R;Ainscough, R.
submitted to the EMBL Data Library, December 1996
A;Reference number: Z19601
A;Accession: T22693
A;Accession: T22693
A;Accession: T22693
A;Accession: Library, translated from GB/EMBL/DDBJ
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100.0%; Pred. No. 26;
tive 0; Mismatches
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A;Introns: 15/1; 54/1; 114/1
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Best Local Similarity
Matches 7; Conserval
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A, Gene: CESP: F55B11.4
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C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: E87507
C;Accession: E87507
D; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 99, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C,Accession: T48784

R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, April 2000

A;Reference number: Z24541

A;Accession: T48784

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-166 <SGN>
A;Experimental source: cosmid contig 13E11; strain 74
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                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-150 <STO>
A;Cross-references: GB:AB005673; NID:g13423567; PIDN:AAK24057.1; GSPDB:GN00148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein 13E11.320 [imported] - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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C,Superfamily: Neurospora crassa hypothetical protein 13E11.320
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100.0%; Pred. No. 30;
tive 0; Mismatches
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Pred. No. 33;
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Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 18, 2003, 19:45:04; Search time 23 Seconds (without alignments) 251.491 Million cell updates/sec

US-09-934-586A-2 123 1 MKAVLLALLMAGLALQPGTA......AAILALLPALGLLLWGPGQL 123 Title: Perfect score: Sequence:

Scoring table:

127863 seqs, 47026705 residues

OLIGO Gapop 60.0 , Gapext 60.0

Searched:

0 Word size :

Total number of hits satisfying chosen parameters:

127863

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

S	Description	O43653 homo sapien	mus m	Q38488 bacteriopha	Q05943 streptomyce	₩.	P97714 mus musculu		oryct	P47224 homo sapien	Q91x96 mus musculu	9	P71013 bacillus su	P08620 homo sapien	3 prote	_	P58422 escherichia		Α.		Q9eyy5 klebsiella	P40420 bacillus su	Q50593 mycobacteri	P15555 streptomyce	P13499 rhodobacter	P25118 mus musculu	P22934 rattus norv	P22248 azotobacter	P43518 rhodobacter	Q99pg2 mus musculu	P10583 azospirillu	_	. P06201 salmonella
SUMMARIES	ID	PSCA HUMAN	PSCA_MOUSE	VG12_BPMU	GLNR STRCO	ALAD_RAT	A1AD_MOUSE	A1AD_HUMAN	A1AD RABIT	MSS4 HUMAN	MSS4 MOUSE	MSS4 RAT	LEPT BACSU	FGF4 HUMAN	SOMA PROAN	ER21 CAEEL	GPH ECO57	GPH_ECOLI	GPH SALTI	GPH SALTY	GPH_KLEAE	YCXE BACSU	YI41 MYCTU	DAC STRSQ	GLINA RHOCA	TRIA MOUSE	TRIA RAT	GLNA_AZOVI	GLNA RHOSH	TM11 MOUSE	GLNA_AZOBR	GLNA_ECOLI	GLNA SALTY
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a	ራቲ	75.6	6.5	6.5	6.5	6.5	6.5	6.5	6.5	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7		5.7		5.7	5.7	5.7		5.7	5.7	5.7	•	5.7		5.7	5.7	5.7
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P77958 streptomyce P43794 haemophilus P2581 neisseria g Q9C1p2 pasteurella P93846 sorghum bic P33699 rhizobium m Q9znx6 medicago tr O23736 brassica ju P46309 arabidopais O22493 lycopersico Q951a2 canis famil
GLN1_STRRP GLNA_HAEIN GLNA_PASMU GLNA_PASMU CP51_SORBI EXOT_RHIME GSH1_BRAJU GSH1_BRAJU GSH1_LYCES FMO1_CANFA
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ALIGNMENTS

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Probom; PD003128; Ly-6_CD59; 1.
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VG12_BPMU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 95:1735-1740(1998).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                        | R | InterProj | Largualse | Large | 
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TISSUB=Fetal, and Kidney;
MEDLINE=98132661; PubMed=9465086;
MEDLINE=98132661; PubMed=9465086;
MELER R.E., Gu Z., Watebe T., Thomas G., Szigeti K., Davis E.,
Wahl M., Nisitani S., Yamashiro J., le Beau M.M., Losa M., Witte O.N.
"Prostate stem cell antigen: a cell surface marker overexpressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN PROSTATE: ALSO FOUND IN SPLEEN, LIVER, LUNG, PROSTATE, KIDNEY AND TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.6%; Score 93; DB 1; Length 123; 100.0%; Pred. No. 1.9e-82; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VISKGCSLNCVDDSQDYYVGKKNITCCDTDLCN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-0cT-2001 (Rel. 40, Created)
16-0cT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Prostate stem cell antigen precursor.
                                                                                 TAG. GO:0005886; C:plasma membrane; TAG. GO:0008222; F:tumor antigen; TAS. InterPro; IPR003632; Ly-6_CD59.
InterPro; IPR01526; LY6_UPAR.
EMBL, AF043498; AAC39607.1; -. EMBL, AJ297436; CAB97347.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003632; Ly-6 CD59. InterPro; IPR001526; LY6 \overline{U}PAR. Pfam; PF00021; UPAR_LY6; \overline{L}
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Best Local Similarity 100.v
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MGD; MGI:1919623; Psca.
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                                                                       MIM; 602470;
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P57096;
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                                                                         BY SIMILARITY.
PROSTATE STEM CELL ANTIGEN.
REMOUED IN MATURE FORM (BY SIMILARITY).
UPAR/LY6.
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N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
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SEQUENCE FROM N.A.
Morgan G., Hatfull G., Hendrix R.;
"Genome of bacteriophage Mu and comparison with the Haemophilus influenzae Mu-like prophage FluMu.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae; Mu-like viruses.
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Priess H., Brauer B., Schmidt C., Kamp D.;
"Sequence of the left end of Mu.";
"In Symonds N., Toussaint A., van de Putte P., Howe M.M.
Phage Mu, pp.277-296, Cold Spring Harbor Laboratory Press, New York (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.5%; Score 8; DB 1; Length 176; 100.0%; Pred. No. 2; Artive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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CDA8566F37307ECC CRC64;
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176 AA; 19895 MW; 44E199AAFBC4BE5D CRC64;
SMART; SM00134; LU, 1.
MOSGITE; PS00393; LY6_UPAR; 1.
Antigen; Glycoprotein; Membrane; GPI-anchor; Signal.
SIGNAL BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                             6.5%; Score 8; DB 1;
100.0%; Pred. No. 1.5;
ative 0; Mismatches
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical protein gpl2 (Protein El3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 AA.
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EMBL; AF083977; AAF01089.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                  13443 MW;
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Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21996410; PubMed=12000953; Bentley S.D., Chater R.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Horneby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Hopwood D.A., Batteill B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The Streptomyces coelicolor glnR gene encodes a protein similar to other bacterial response regulators.";
Gene 130:145-150(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
-i- FUNCTION: ACTIVATES THE TRANSCRIPTION OF THE GLNA GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sensory transduction; Phosphorylation; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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MOD RES 50 50 PHOSPHORYLATION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 267;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                      OCT-1994 (Rel. 30, Created)
01-CCT-1994 (Rel. 30, Last sequence update)
Table-ED-2003 (Rel. 4), Last annotation update)
Transcriptional regulatory protein glnR.
GINR OR SCO4159 OR SCD84.26C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.5%; Score 8; DB 1;
100.0%; Pred. No. 2.7;
ive 0; Mismatches
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EMBL, AL933119; CAB88492.1; -.
PIR; N00831; JN0083.
HSSP; P08402; 1QQ1.
InterPro; IRR001867; Trans_reg_C.
Pfam; PF00486; trans_reg_C_1.
Probom; PD000329; Trans_reg_C.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=A3(2);
MEDLINE=93345814; PubMed=7688332;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wray L.V. Jr., Fisher S.H.;
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nes 8; Conservative
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                                   115 ALLPALGL 122
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STRAIN=A3(2) / M145;
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Q05943;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=9514877; PubMed=7815325,
A Schwinn D.A., Johnston G.I., Page S.O., Mosley M.J., Wilson K.H.,
Schwinn D.A., Johnston G.I., Page S.O., Mosley M.J., Wilson K.H.,
A Parry-Smith D.J., Peter B., Bailey D.S.,
I "Cloning and pharmacological characterization of human alpha-1
adrenergic receptors: sequence corrections and direct comparison with
I adrenergic receptors: sequence corrections and direct comparison with
The species homologues.",
I J. Pharmacol. Exp. Ther. 272:134-142(1995).
I J. SUBCELUIAR INCOMENTIAL COUPLED RECEPTORS.
I J. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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EMBL; M60654; AAA63477.1,

EMBL; M60654; AAA63477.1,

DR PRE; A38731; A38731.

DR PROSITE; PRO0027; GPCR.Rhodpsn.

DR PROSITE; PS00237; GPCRRHODDPSN.

DR PROSITE; PS00237; GPCRTEN RECEP_F1_1; 1.

DR PROSITE; PS00236; GPROTEIN RECEP_F1_2; 1.

KW Multigene family; Phosphorylation; Lipoprotein; KW Multigene family; Phosphorylation; Lipoprotein; Panksmem 91 115 CYTOPLASMIC (POTENTIAL).

""MAIN 116 127 CYTOPLASMIC (POTENTIAL).

""MAIN 128 153 2 (POTENTIAL).

154 163 3 (POTENTIAL).

4 (POTENTIAL).

4 (POTENTIAL).

177. CYTOPLASMIC (POTENTIAL).

186 3 (POTENTIAL).

4 (POTENTIAL).

187. CYTOPLASMIC (POTENTIAL).

188. CYTOPLASMIC (POTENTIAL).

199. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lomasney J.W., Cotecchia S., Lorenz W., Leung W.-Y., Schwinn D.A., Yang-Feng T.L., Brownstein M., Lefkowitz R.J., Caron M.G.; "Molecular cloning and expression of the cDNA for the alpha 1A-adrenergic receptor. The gene for which is located on human chromosome 5.";
                                                    01-MAR-1992 (Rel. 21, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 32, Last annocation update)
30-MAY-2000 (Rel. 39, Last annocation update)
Alpha-1D adrenergic receptor (Alpha 1D-adrenoceptor) (Alpha-1A adrenacyic receptor) (RA42).
ADRALD OR ADRALA.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
   561 AA
                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Sprague-Dawley; TISSUE=Brain cortex; MEDLINE=91177889; PubMed=1706716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Biol. Chem. 266:6365-6369(1991).
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
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368
375
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TRANSMEM
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TRANSMEM
DOMAIN
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CARBOHYD
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        N-LINKED (GLCNAC. ) (POTENTIAL).

PALMITATE (POTENTIAL).

GLY-ARCH.

AVGHWASTGDARSDCAPSPRIAPPGAPLALTAHPGAGS

ADTPETQDSVSSSRKPASA -> SLRPPLASLDRRRAFRLR

POPSHRSPRGPSSPHCTPGCGLGRRAGDAGFGLQQSKASLR
                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
MEDLINE=96064018; PubMed=7595531;
Alonso-Liamazares A., Zamanillo D., Casanova B., Ovalle S., Calvo P.,
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDILINE=20085927; PubMed=10622215;
Arai K., Tanoue A., Goda N., Takeda M., Takahashi K., Tsujimoto G.;
"Characterization of the mouse all-adrenergic receptor gene.";
Jpn. J. Pharmacol. 81:271-278(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Testis
MEDLINE-94116980; PubMed=828818;
MEDLINE-94116980; PubMed=8288218;
MILL T.M., Chen Y., Gilbert D.J., Moore K.J., Yu L., Simon M.I.,
Copeland N.G., Jenkins N.A.;
"Identification, chromosomal location, and genome organization of
mammalian G-protein-coupled receptors.";
Genomics 18:175-184(193)
-:- FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS EFFECT
THROUGH THE INPLUX OF EXTRACELLULAR CALCIUM.
-:- SUBCELLULAR LOCATION: Integral membrane protein.
-:- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
 N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                        P97714; Q61619;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FBB-2003 (Rel. 31, Last annotation update)
Alpha-1D adrenergic receptor (Alpha 1D-adrenoceptor) (Alpha-1A adrenoceptor)
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chinchetru M.A.; "Molecular cloning of alpha ld-adrenergic receptor and tissue distribution of three alpha 1-adrenergic receptor subtypes in
                                                                                                                               Length 561;
                                                                                                                                                        0; Indels
                                                                                             (IN REF. 1).
B6537DCAD4F7BE27 CRC64;
                                                                                                                                Score 8; DB 1;
Pred. No. 4.9;
                                                                                                                                                                                                                                                                  562 AA
                                                                                                                               Query Match 6.5%; Score 8; DB 1
Best Local Similarity 100.0%; Pred. No. 4.9
Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                  . PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nouse.";
J. Neurochem. 65:2387-2392(1995).
                                                                                                        561 AA; 59354 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 190-350 FROM N.A.
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                                                                                                                                                                                                                                                                  STANDARD;
60
76
413
57
423
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                                 DOMAIN
DOMAIN
CONFLICT
           CARBOHYD
LIPID
                                                                                                         SEQUENCE
CARBOHYD
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Bruno J.F., Whittaker J., Song J., Berelowitz M.; "Molecular cloning and sequencing of a cDNA encoding a human alpha lA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

S (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

T (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . . ) (POTENTIAL).

N-LINKED (GLCNAC. . . ) (POTENTIAL).

PALMITATE (POTENTIAL).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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MEDINDE=94239386; PubMed=8183249;
Forray C., Bard J.A., Wetzel J.M., Chiu G., Shapiro E., Tang R..
Lepor H., Harrig P.R., Weinshank R.L., Branchek T.A.,
Gluchowski C.;
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01-NOV-1995 (Rel. 32, Last sequence update)
11-OCT-2001 (Rel. 40, Last annotation update)
Alpha-1D adrenergic receptor (Alpha 1D-adrenoceptor) (Alpha-1A ADRALD OX PARALA.
                                                                                                                                                                                   PROSITE; PS00237, G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1 2; 1.
G_protein coupled receptor; Transmembrane; Glycoprotein;
Multigene family; Phosphorylation; Lipoprotein; Palmitate.
DOMAIN 91 115 1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.5%; Score 8; DB 1; Length 562;
100.0%; Pred. No. 4.9;
tive 0; Mismatches 0; Indels
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R -> G (IN REF. 3).
6CF15515B5F7FA47 CRC64;
                                                                                                                                                                                                                                                                                                          1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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EMBL; AB030641; BAA90312.1; JOINED.
                                                                                    MGD; MGI:106673; Adrald.
InterPro; IPR000276; GPCR_Rhodpsn.
PROMO1, 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
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       ымыр; 120333; AAA16854.1; -.
PIR; D48909; D48909.
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Best Local Similarity 100.
Matches 8; Conservative
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562 AA;
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GO; GO:0004937; F:alphal-adrenergic receptor activity; TAS.
GO; GO:0008283; P:cell proliferation; TAS.
GO; GO:0007287; P:cell-cell signaling; TAS.
GO; GO:0007275; P:DNA metabolism; TAS.
GO; GO:0007286; P:DNA metabolism; TAS.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.
GO; GO:0007188; P:G-protein signaling, coupled to cAMP nucleo. .; TAS.
GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
FREM: PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                   adrenergic receptors: sequence corrections and direct comparison with
contraction in human prostate has the pharmacological properties of the cloned human alpha 1c subtype.";

Mol. Pharmacol. 45:703-708(1994).
                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94296402; PubMed=8024574;
Weinberg D.H., Trivedi P., Tan C.P., Mitra S., Perkins-Barrow A.,
Borkowski D., Strader C.D., Bayne M.;
"Cloning, expression and characterization of human alpha adrenergic
receptors alpha la, alpha lb and alpha 1c.";
Biochem. Biophys. Res. Commun. 201:1296-1304(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Placents, and Prostate;
MEDLINE=95266059; PubMed=7746284;
MEDLINE=95266059; PubMed=7746284;
Minneman K.P., Hirasawa A., Tsujimoto G., Tanaka T., Yano J.,
Minneman K.P., Murphy T.J.;
"Cloning of the human alpha 1d-adrenergic receptor and inducible expression of three human subtypes in SK-N-MC cells.";
Mol. Pharmacol. 47:977-986(1995).
-!-FUNCTION: THIS ALPHA-ADRENERGIC RECEPTOR MEDIATES ITS EFFECT THROUGH THE INPLUX OF EXTRACELLULAR CALCIUM.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=91114877; PubMed=7815325;
Schwinn D.A., Johnston G.I., Page S.O., Mosley M.J., Wilson K.H.
Worman N.P., Campbell S., Fidock M.D., Furness L.M.,
Parry-Smith D.J., Peter B., Bailey D.S.;
"Cloning and pharmacological characterization of human alpha-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; it...
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR0237; GFCRRHODOPSN.
PROSITE; FS00237; G PROTEIN RECEP F1 1; 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; G-protein coupled receptor; Transmembrane; Glycoprotein; G-protein coupled receptor; Transmembrane; Glycoprotein; G-protein; Phosphorylation; Lipoprotein; Palmitate.

EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
                                                                                                                                                                                                                                                                       other species homologues.";
J. Pharmacol. Exp. Ther. 272:134-142(1995)
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EMBL; U03864; AAB60351.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L31772; AAB59487.1; -. S70782; AAB31163.2; -.
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EMBL; D29952; BAA06222.1;
PIR; J19389; 139369.
PIR; JH0447; JH0447.
Genew; HGNC:280; ADRAID.
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                                                                                                                                                                                                PAVGGVPGGAGGGGVVGAGSGEDNRSSAGEPGSAGAGD
VNG -> MAAALRSVMMAGYLSEWRTPTYRSTEMVQRLRM
EAVQHSTS (IN REF. 1).
                                                                                                                                                                                   MTFRDLLSVSFEGPRPDSSAGGSSAGGGGSAGGAAPSEG
                                                                                                                                                                                                                                          S -> G (IN REF. 4).
KPPSAFREWRLLGPFRRPTTQLRAKVSSLSHKIRAGGAQR
                                                                                                                                                                                                                                                                       AEAACAQRSEVEAVSLGVPHËVAEGATCQAYELADYSNLR
ETDI -> SHPAPSASGGCWGRSGDPRPSCAPKSPACRTR
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Suzuki F., Miyamoto S., Takita M., Oshita M., Watanabe Y.,
Kakizuka A., Narumiya S., Taniguchi T., Muramatsu I.;
"Cloning, functional expression and tissue distribution of rabbit
alpha 1d-adrenoceptor.";
Biochim. Biophys. Acta 1323:6-11(1997)
-!- FUNCTION: THIS ALPHA-ADRENBERGIC RECEPTOR MEDIATES ITS EFFECT
THROUGH THE INFLUX OF EXTRACELLULAR CALCIUM.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                   SPPGARSAQRQRAPSAQRWRLCP (IN REF. 1).
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EBEB134CF20A4988 CRC64;
EXTRACELLULAR (POTENTIAL)
                                              4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                   5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  002656;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Alpha-1D adrenergic receptor (Alpha 1D-adrenoceptor).
                   3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                          7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                      PALMITATE (POTENTIAL)
                                        4 (POTENTIAL)
                                                                                                                                                                                                                              EAVQHSTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                  522 522 R
572 AA; 60462 MW;
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Matches 8; Conservative
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213 AAAILALL 220
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31
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DOMAIN
TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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MEDLINE-22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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P47224, Q02929.
O1.FEB-1996 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annocation update)
Guanine nucleocide exchange factor MSS4 (Rab interacting factor)
RABIF OR RASGRF3 OR MSS4.
                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                             Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 576;
G_PROTEIN_RECEP_F1_1; 1.
G_PROTEIN_RECEP_F1_2; 1.
receptor; Transmenbrane; Glycoprotein;
Phosphorylation; Lipoprotein; Palmitate
101
EXTRACELLUIAR (POTENTIAL).
126
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
                                                                                                       2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
3 (POTENTIAL).
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                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL)
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87
424
54
78
78
427
576 AA;
 PROSITE, PS00237, G
PROSITE, PS50262, G
G-protein coupled r
Multigene family, P
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Best Local Similarity
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257
281
3354
3354
386
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A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A Stapheton M., Soares M.B., Bonaldo M.F., Rubin G.M., Hong L.,
Stapheton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Friby J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
Redenarion and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95379975; PubMed=7651540;
Yu H., Schreiber S.L.;
"Structure of guainine-nucleotide-exchange factor human Mss4 and identification of guainine-nucleotide exchange surface.";
Nature 376:788-791(1995).
-!-FUNCTION: GUANINE-NUCLEOTIDE-RELEASING PROTEIN THAT ACTS ON MEMBERS OF THE SCE4/YPTI/RAB SUBFAMILY. STIMULATES GDP RELEASE FROM BOTH YPTI AND RABBA, BUT IS LESS ACTIVE ON THESE PROTEINS
THAN ON THE SEC4 PROTEIN. MIGHT PLAY A GENERAL ROLE IN VESICULAR
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MIM, 603417; -.

GO; GO:0005085; P:guanyl-nucleotide exchange factor activity; TAS.
GO; GO:0006944; P:membrane fusion; TAS.
GO; GO:0006899; P:non-selective vesicle transport; TAS.
Pfam; PF04421; M884; 1.
Guanine-nucleotide releasing factor; Protein transport; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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-!- SIMILARITY: BELONGS TO THE DSS4/MSS4 FAMILY.
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EMBL; U74324; AAB18264.1; -.
EMBL; BC018488; AAH18488.1; -.
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PDB; 1FWQ; 04-OCT-00
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STRUCTURE BY NMR
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MSS4_RAT
    STTTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Straubberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A Straubberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Richald S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moorer T., Max S.I., Wang J., Hsieh F.,

Biatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Branchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Tonshiyuki S., Caraninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Glubs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Rhich Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N. Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences.";

"Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences.";

"FWON BOTH YPTI AND RABBA, BUT IS LESS ACTIVE ON THESE PROTEINS

"THAN ON THE SCE4/YPTI/RAB SUBFAMILY. STIMULATES GDP RELEASE

FROM BOTH YPTI AND RABBA, BUT IS LESS ACTIVE ON THESE PROTEINS
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15-SEP-2003 (Rel. 42, Last annotation update)
Guanine nucleotide exchange factor MSS4 (Rab interacting factor):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Guanine-nucleotide releasing factor, Protein transport, Zinc.
                                                                                                                                                                            Length 123;
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                                                                                                                              13839 MW; 78E98395FAE10257 CRC64;
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SIMILARITY: BELONGS TO THE DSS4/MSS4 FAMILY.
                                                                                                                                                     5.7%; Scc... No. - 100.0%; Pred. No. - 0; Mismatches
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MEDLINE=22388257; PubMed=12477932;
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28-FEB-2003 (Rel. 41, Last sequ
15-SEP-2003 (Rel. 42, Last anno
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MSS4 MOUSE
D MSS4 MOUSE
AC 091X36;
DT 28-FEB-2003
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DT 15-SEP-2003
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RA KLAUSHER F. F.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAINE-Sprague-Dawley, TISSUE-Brain;
MEDLINE-93156814; PubMed-8429887;
MEDLINE-93156814; PubMed-8429887;
Burton J., Roberts D., Montaldi M., Novick P., de Camilli P.;
"A mammalian guanine-nucleotide-releasing protein enhances function of yeast secretory protein Sec4.";
Nature 361464-467(1993).
Nature 361464-467(1993).
                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (Rel. 31, Created)
1-FEB-1995 (Rel. 31, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Guanine nucleotide exchange factor MSS4 (RAB interacting factor).
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Guanine-nucleotide releasing factor; Protein transport; Zinc;
                                                                                                                   Length 123;
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ZINC (BY SIMILARITY).

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73F3AEECODBE8B02 CRC64;
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SIMILARITY).
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-!- SIMILARITY: BELONGS TO THE DSS4/MSS4 FAMILY.
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                                                                                                                                                          0; Mismatches
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13915 MW;
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Matches 7; Conservative
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PDB; 1HXR; 04-APR-01.
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Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
A porrise R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Brian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
A penizot F., Pulita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
A duiseppi G., Guy B.J., Hajech Y., Haiech J., Harwood C.R., Henaut A.,
Hilbert H., Holaappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
Medina N., Mellado R.P., Liu H., Masuda S., Mauel C., Medigue C.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Signal peptidase I T (EC 3.4.21.89) (SPase I) (Leader peptidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=168;
Tjalsma H., Bolhuis A., Bron S., Venema G., van Dijl J.M.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1423,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Winters P., Caldwell B.M., Enfield L., Ferrari E.; "The ampS.nprE (124 degrees.127 degrees) region of the subtilis 168 chromosome: sequencing of a 27 kb segment identification of several genes in the area."; Microbiology 142:3033-3037(1996).
                                                                                                                                                                                                                                                                                                                  13928 MW; ACB7D07E2735811C CRC64;
                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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Pred. No.
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MEDLINE=97124187; PubMed=8969500;
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LQPGTAL 37
                                                                                                                                                                                                                                                                                                                                                                                                                                         LOPGTAL 21
                                                                                                                                                                                                                                                                                                                      123 AA;
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P71013;
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Best Local S
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Parecoru V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Scriguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Wadlut R., Wadler E., Wedler E., Weller H., Wellzengger T., Yakamoto K., Yakamo
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01-AUG-1988 (Rel. 08, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-Bat growth factor-4 precursor (RGP-4) (Heparin secretory
transforming protein) (HST-1) (HST) (Transforming protein KS3) (HBGF-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 390:249-256(1997).

-!- CATALYTIC ACTIVITY: Cleavage of N-terminal leader sequences from
-!- CATALYTIC ACTIVITY: The precure of the protein (Potential).
-!- SUBCELLUTA LOCATION: Type II membrane protein (Potential).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY $26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukono saprazio interiora del Craniata; Vertebrata; Euteleostomi;
Rammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Fransmembrane; Hydrolase; Protease; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL) POTENTIAL.
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BY SIMILARITY
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InterPro; IPR000223; SigPrase_S26A.
Pfam; PR00461; Peptidase_S26; 1.
PRINTS; PR00727; LEADERPTASE.
PROSITE; PS00501; SPASE 1 1; 1.
PROSITE; PS00760; SPASE 1 2; 1.
PROSITE; PS00761; SPASE 1 2; 1.
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nes 7; Conservative
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206 AA.

STANDARD;

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073848;
28-FEB-2003
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Q09473;
  SOMA_PROAN
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SEQUENCE
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ER21_CAEEL
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb.sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: CAN TRANSFORM NIH 3T3 CELLS FROM A HUMAN STOWACH TUMOR (HST) AND FROM KARPOSI'S SARCOMA (KS3). IT HAS A MITOGENIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                 "cDNA sequence of human transforming gene hst and identification of
the coding sequence required for transforming activity.";
Proc. Natl. Acad. Sci. U.S.A. 84:2980-2984(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005576; C:extracellular; TAS.
GO; GO:0008083; F:growth factor activity; TAS.
GO; GO:0007048; P:cell-cell signaling; TAS.
GO; GO:0007048; P:oncogenesis; TAS.
GO; GO:000228; P:posttive regulation of cell proliferation; TAS.
GO; GO:0007165; P:signal transduction; TAS.
                                                                                                                               "Genomic sequence of hst, a transforming gene encoding a protein homologous to fibroblast growth factors and the int-2-encoded
                                                                                       foshida T., Miyagawa K., Odagiri H., Sakamoto H., Little P.F.R.,
Terada M., Sugimura T.;
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0
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MEDLINE=87301716; Pubmed=2957062;
Delli Bovi P., Curatola A.M., Kern F.G., Greco A., Ittmann M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE, PS00247, HBGF FGF; 1.
Proto-oncogene, Growth factor; Mitogen; Signal; 3D-structure.
                                                                                                                                                                                                                                                            MEDLINE-87204251; PubWed-2953031;
Taira M., Yoshida T., Miyagawa K., Sakamoto H., Terada M.,
Sugimura T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.7%; Score 7; DB 1; Length 206;
100.0%; Pred. No. 20;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 84:7305-7309(1987)
                                                                   MEDLINE=88041096; PubMed=2959959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00262; ILLHBGF.
ProDom; PD000831; ILL HBGF; 1.
SMART; SM00442; FGF; 1.
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EMBL; M17446; AAAS9473.1; -.
PIR; A28417; TVHUHS.
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Best Local Similarity 100...
7; Conservative
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Genew; HGNC:3682; FGF4.
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                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                         SEQUENCE FROM N.A.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genew; HGNC:
MIM; 164980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                               protein
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                May D., Alrubaian J., Patel S., Dores R.M., Rand-Weaver M.; "Studies on the GH/SL gene family: cloning of African lungfish (Protopterus annectens) growth hormone and somatolactin and toad (Bufo
                                                                                                                                                                                                                                                                                                                                                                                             marinus) growth hormone.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Growth hormone plays an important role in growth control
and is involved in the regulation of several anabolic processes.
Implicated as an osmoregulatory substance important for seawater
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda, Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                          Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          adaptation.
--- SUBCELLULAR LOCATION: Secreted.
--- SIMILARTY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eut
Dipnoi, Lepidosireniformes, Protopteridae, Protopterus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOMATOTROPIN.
BY SIMILARITY.
BY SIMILARITY.
9ED9D1E3BC307B57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative ER lumen protein retaining receptor C28H8.4.
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Somatotropin precursor (Growth hormone).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00103; hormone; 1.
PROSITE; PS00266; SOMATOTROPIN 1; FALSE NEG.
PROSITE; PS00338; SOMATOTROPIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.7%; Score 7; DB 1,
100.0%; Pred. No. 20;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 AA
                                                                                                                                 Protopterus annectens (African lungfish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF062745; AAC16496.1; -. HSSP; P01241; 1HUW.
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SIGNAL 1 22
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nes 7; Conservative
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Miller N., Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                               TISSUE=Pituitary;
                                                                                                                                                                                                               NCBI_TaxID=7888;
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14 AVLLALL 20

RESULT 14 SOMA_PROAN

3 AVLLALL 9

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Required for the retention of luminal endoplasmic reticulum proteins. Determines the specificity of the luminal ER protein refention system. Also required for normal vesicular traffic through the Golgi (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                       EMBL; U20861; AAA62292.1; -.
PIR; H88469; H88469.
WOTMPEP; C28H8.4; CE01826.
InterPro; IPRR000133; ERRet_receptor.
Pfam; PF00810; ER lumen_recept; 1.
PRINTS; PR00650; ERLUMENR.
PRODOM; PD005774; ERLUMEN RECEPTOR.; 1.
PROSITE; PS00952; ER_LUMEN RECEPTOR.1; 1.
PROSITE; PS00952; ER_LUMEN_RECEPTOR.2; 1.
Hypothetical protein; Endoplasmic reticulum; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.7%; Score 7; DB 1; Length 213;
100.0%; Pred. No. 21;
ive 0; Mismatches 0; Indels
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LUMBIAL (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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Best Local Similarity
Matches 7; Conserv
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DOMAIN
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Search completed: August 18, 2003, 19:54:58 Job time : 24 secs

104 AAILALL 110 ||||||| 102 AAILALL 108

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Q93bc1 salmonella Q93bh2 salmonella Q93be4 salmonella Q93bd4 salmonella salmonella salmonella salmonella

Perfect score:

Run on:

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Scoring table:

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Database :

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Gaps

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3 AVLLALLMA 11

Q956RS Q9KIM3 Q8GQY9 Q8GQYS

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"Inverse alpha(1A) and alpha(1D) adrenoceptor mRNA expression during isolation of hepatocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                              EUT. J. Pharmack. 234:21-237 (1999).

-1. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

-1. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. EMBL; AF108017; AAD22541.1; -

INTER-PRO; IPRO00276; GPFCR. Rhodpsn.

Pfam; PF00001; 7tm 1; 1.

PROSITE; PS00237; G-PROTEIN RECEP F1 1; 1.

PROSITE; PS00237; G-PROTEIN RECEP F1 2; 1.

G-protein coupled receptor; Receptor; Transmembrane.
                                                                                                                                                        Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                        Gonzalez-Espinosa C., Romero-Avila M.T., Mora-Rodriguez D.M.,
Gonzalez-Espinosa D., Garcia-Sainz J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 AA; 15185 MW; 59AF5E8D5E1DDEF6 CRC64;
                                                                Last sequence update)
Last annotation update)
                                                                                                               Alpha-1D adrenergic receptor (Fragment)
                                        01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last seq
01-OCT-2002 (TrEMBLrel. 22, Last ann
                                                                                                                                                                                                                                                                                                  TISSUE=Liver;
MEDLINE=20079491; PubMed=10611446;
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Matches 8; Conservative
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PRELIMINARY;
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NON TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Azakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Saito T., Okazaki Y., Gojobori T., Rosukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H., Sasishi K., Matsudo Y., King B., Kochhua H., Aschriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Bardarelli R., Barsh G., Braka K., Dolunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Nordone P., Marchionni L., Mashima J., Mazzarelli J., Mambaerts P., Asasaki H., Saro K., Schoren R., Shibara Y., Sakonto N., Sazuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hashahizaki Y., Rhunctional annotation of a full-length mouse cDNA collection.";
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"Murine six-transmembrane epithelial antigen of the prostate, prostate stem call antigen, and prostate-specific membrane antigen: prostate-specific cell-surface antigens highly expressed in prostate cancer of transgenic adenocarcinoma mouse prostate mice.";

transgenic adenocarcinoma mouse prostate mice.";

EMBL; AK008851; BAB25929.1;

EMBL; AK008851; BAB25929.1;

EMBL; AK008851; BAB25929.1;

InterPro; IPR003522; Ly-6 CD59.

InterPro; IPR003532; Ly-6 CD59.

InterPro; IPR001528; Ly-6 UPAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             00983; LYG UPAR; 1.
123 AA; 13477 MW; 67AB566F3D30797A CRC64;
                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
101-MAR-2003 (TrEMBLrel. 23, Last annotation update)
22.10408904Rik protein (Prostate stem cell antigen).
PSCA OR 2210408904RIK.
                                                                                                                  123 AA
                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J; TISSUE=Stomach;
MEDLINE=21085660; Pubmed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=21371909; PubMed=11479226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam, PF00021; UPAR LY6, 1.
ProDom, PD003128; LY-6 CD59; 1.
SMART; SM00134; LU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
                                                                                                                  PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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SEQUENCE 123 AA;
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RESULT 2
09D70
DT 01-4
DT 01-1
DE PSC10
CC Manma
CC Manm

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Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
Tshirin T., Riggs F., Lismann V., Blunt S., Pai G.,
Vanaken S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbush J.,
Salzberg S.L., White O., Fraser C.M.;
"Oryza sativa chromosome 3 BAC OSJNBb0048D20 genomic sequence.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AC084766; AAL82515.1;
Gramene; Q68767;
                                                                           Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (Rice).
Wkaryota, Virtdiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
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6.5%; Score 8; DB 11; Length 140;
100.0%; Pred. No. 7.7;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 167.AA; 18582 MW; 11C5F3EA7341BEF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JOCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical 18.6 kDa protein.
0SJNBB0048D20.6.
                                                                                                                                                                                                                                                                                                                                                                                    167 AA.
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Best Local Similarity
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RESULT 3 Q9WU26

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Local Similarity 100.
nes 8; Conservative
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NCBI_TaxID=29459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                       103 AAAILALL 110
                                                                                                                                                                                                                                                 262 AAAİLALL 269
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K01A6.4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239;
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Q21073;
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Matches
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Kishida Y., Kiyokawa C., Kohara M., Matsumoco M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.,
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN=1330 / Biovar 1;

STRAIN=1330 / Biovar 1;

MEDLINE=22247741; Dubmed=12271122;

Raulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,

Rad T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,

Baugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,

Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.

Riedmuller S., Tetelin H., Gill S.R., White O., Salzberg S.L.,

Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;

"The Brucella suis genome reveals fundamental similarities between animal and plant pathogens and symblonts.";

Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
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                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
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Pred. No. 12;
  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 protein; Complete proteome.
249 AA; 25285 MW; 5B70922CEEA5703C CRC64;
                                                                                                                                                                                                                          01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-0AR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein mll2193.
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Conserved hypothetical protein.
  ;
                                                                                                                                                                                                     249 AA
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Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                         Rhizobium loti (Mesorhizobium loti).
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                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
8; Conservative
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NCBI_TaxID=29461;
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                                            102 PAAAILAL 109
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                                                                                    134 PAAAILAL 141
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QBFY23

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DT 01-M

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                          Length 279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 284;
                                                                                                                                                                            0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cottage A.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; AE014494; AAN30957.1; -.
TIGR; BR2067; -.-
Hypothetical protein; Complete proteome.
SEQUENCE 279 AA; 30481 NW; 452110EFCD636FA5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27053 MW; C5A748D8E72DE82D CRC64;
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Last annotation update)
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ATP/GTP-binding protein.
                                                                                                                          DB 16;
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                                                                                                                                                                                                                                                                                                                                                                                                          284 AA.
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0; Mismatches
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                                                                                                                          6.5%; Score 8; DB 1
100.0%; Pred. No. 14;
                                                                                                                                                                            0; Mismatches
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MEDLINE=20020109; PubMed=11756688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              investigating biology.";
Science 283:2012-2018(1998).
EMBL, 268750; CAA92963.1; -.
WormPep; KOIA6.4; CE06637.
SEQUENCE 284 AA; 27053 MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                Query Match
Best Local Similarity 100...
Fines 8; Conservative
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RESULT 9 Q9H1N4

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structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO NADH-UBIQUINONE/PLASTOQUINONE (COMPLEX I), VARIOUS CHAINS.
                    Pyrococcus abyssi genome sequence: insights into archaeal chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fattus sp.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOI. Pharmacol. 40:876-883(1991).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
Interpro; IPR000216; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=92100054; PubMed=1661838;
Perez D.M., Piascik M.T., Graham R.M.;
"Solution-phase library screening for the identification of rare clones: isolation of an alpha 1D-adrenergic receptor cDNA.";
                                                                                                                                                                                                                                                                                 6.5%; Score 8; DB 17; Length 486; 100.0%; Pred. No. 22; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.5%; Score 8; DB 11; Length 559; 100.0%; Pred. No. 25;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Alpha 1-adrenergic receptor subtype alpha 1D, alpha 1D-AR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                   EMBL; AJ248287; CAB50381.1; -.
InterPro; IPR003916; NAPHub_oxred5.
InterPro; IPR00150; Oxidored_q1.
Pfam; PF00361; oxidored_q1; 1.
PRINTS; PR01494; NAPHDHGNASE5.
SEQUENCE 486 AA; 53669 WW; BC996E4F6A0CSCBA CRC64;
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PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Receptor; Transmembrane.
SEQUENCE 559 AA; 59739 MW; 37CD9BD6969D3A47D CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             559 AA.
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0; Mismatches
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ALPHA-1D.
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Best Local Similarity 100.
Matches 8; Conservative
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les 8; Conserv
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    SWRDBRCCCRTTB
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
BA137P16.1 (Adrenergic, alpha-1D-, receptor (Alpha 1D-adrenoreceptor))
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Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
Pyrococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kammany H.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
EMBL; AL357040; CAC17424.1; -.
InterPro: IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                             ;
0
genome sequence of the facultative intracellular pathogen
                                                                                                                                                                                   DB 16; Length 299;
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                                                                                                                                            299 AA; 32663 MW; 9312097D1C525123 CRC64;
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PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS0026; G_PROTEIN_RECEP_F1_2; 1.
G_PROCEIN coupled receptor; Receptor; Transmembrane.
NON_TER 370 AA: 370.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hydrogenase-4 component D (EC 1.....).
                Brucella melitensis.";
Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
EMBL; AE009638; AALS3241.1;
                                                                                                                                                                               6.5%; Score 8; DB 16
100.0%; Pred. No. 15;
tive 0; Mismatches
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                                                                         InterPro, IPRO05177; DUF299, DFam; PF03618; DUF299, 1.
Complete proteome. SEQUENCE 299 AA; 32663 MW
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RESULT 10

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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of cordered cosmids and a detailed genetic and physical map for the B Mb Streptomyces coelicalor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21996410; PubNed=12000953; MEDLINE=21996410; PubNed=12000953; Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Rabbinowitsch E., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                          Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Streptomycineae, Streptomycetaceae, Streptomyces.
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01-WAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Sub-unit III of an aa3-type cytochrome oxidase (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=A3(2);
Bentley S.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                   Kormanec J., Sevcikova B., Homerova D.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                           Brown S.P., Harris D.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 AA; 6276 MW; F3D69CEE87375643 CRC64;
                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 23, Last annotation update)
F23a (Hypothetical 6.3 kDa protein)
F23A OR SCO4189 OR 2SCD46.03C.
 62 AA.
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MEDLINE=97000351; PubMed=8843436;
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EMBL; AF230488; AAF82057.1; -.
EMBL; AL939119; CAC04025.1; -.
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hes 7; Conservative
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                                                                                                                           Streptomyces coelicolor
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STRAIN=A3(2), AND M145;
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Lepidosauria, Squamata, Iguania, Iguanidae, Iguaninae, Iguana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21190842; PubMed=11297180; Janke A., Erpenbeck D., Nilsson M., Arnason U.; Janke A., Erpenbeck D., Nilsson M., Arnason U.; The mitochondrial genomes of the iguana (Iguana iguana) and the caiman (Caiman crocodylus): Implications for amniote phylogeny."; Proc. R. Soc. Lond., B, Biol. Sci. 268:623-631(2001).
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EBBL; JAZ7 (SIJ1, CAC37093.1; -
InterPro; IPR003916; NADHUD_oxred5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01434; NADHDHGNASES.
NAD; Oxidoreductase; Ubiquinone; Mitochondrion.
SEQUENCE 602 AA; 66177 MW; 820FAF8A2D4CD92B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
NADH dehydrogenase subunit 5.
                                                                                                                                                                                                                                                                                                                        DB 6;
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100.0%; Pred. No. 26;
ive 0; Mismatches
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100.0%; Pred. No. 25;
tive 0; Mismatches
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nterPro; IPR001516; Oxidored q1_N.
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Pfam; PF00662; oxidored_q1_N;
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nes 8; Conservative
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NCBI_TaxID=9823;
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RESULT 13
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Matches

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RESULT 14 Q9KIM3

Gaps

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Indels

Taylor K.,

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GN COXC.

OS Thiobacillus ferrooxidans.

OX Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillus.

OX NCBI_TAXID=920;

RN [1] TAXID=920;

RN $EQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RA SASAKI K., Ida C., Matsumoto N., Ando A., Saiki H., Ohmura N.;

RT "Respiratory isozyme, two types of rusticyanin of Acidithiobacillus

RT Ferroxidans.";

RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

BL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ catabases.

BL Submitted (OCT-2002) to the BMBL/GenBank/DDBJ catabases.

CLE Submitted (OCT-2002) to the EMBL/GenBank/DDBJ catabases.

RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ catabases.

RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ catabases.

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RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ catabases
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Search completed: August 18, 2003, 19:56:43 Job time : 99 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

August 18, 2003, 19:32:04; Search time 23 Seconds (without alignments) 251.491 Million cell updates/sec Run on:

US-09-934-586A-2 646 1 MKAVLLALLMAGLALQPGTA......AAILALLPALGLLLWGPGQL 123 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched:

127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Mach 0% Maximum Macch 100% Listing first 45 summaries

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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*	Query Match	99.8	60.1	Ġ.	4.	ς.	19.5	•	17.9	17.7	17.3		15.6	15.4	4.	14.9	14.7	14.7	4	4.	14.6	14.4	14.3	14.3	14.1		13.9	•				13.7	13.5	13.4
	Score	645	388		158.5	144	126	121.5	115.5	114.5	111.5	н	0	٥.	•	96.5	95	95	95	94.5	94	93	92.5		91	91	90	89.5	ď.	89	89	88.5	87	86.5
	Result No.	-1	~	м	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59	30	31	32	33

P51447 actus trivi O9wv67 mus musculu O9w/k1 pseudonaja O9gxn2 rattus norv P17696 dendroaspis P18328 dendroaspis P18328 dendroaspis O9w7k0 pseudonaja O22963 bungarus mu Q95126 bos taurus Q2816 cercopithec O9w7k2 pseudonaja O9ygjo bungarus mu
CD59 AOTTR LY61 MOUSE. NX52 PSETE RXP1 RAT TSYL DENAN NX83 PSETE NXH6 BUNMU AVRB BOVIN CD59 CERAE NXS1 PSETE NXS1 PSETE
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128 134 134 134 134 136 128 128 128 128 128
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ALIGNMENTS

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TISSUB=Fetal, and Kidney;
MEDLINE=98132661; PubMed=9465086;
MEDLINE=98132661; PubMed=9465086;
Reiter R.E., Gu Z., Matabe T., Thomas G., Szigeti K., Davis E.,
Wahl M., Nisitani S., Yamashiro J., le Beau M.M., Losa M., Witte O.N.;
"Prostate stem cell antigen: a cell surface marker overexpressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN PROSTATE. ALSO FOUND IN SPLEEN, LIVER, LUNG, PROSTATE, KIDNEY AND TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
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BY SIMILARITY.
BY SIMILARITY.
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N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
GPI-ANCHOR (POTENTIAL).
                                                                                                                                                                                                                                                       PROSTATE STEM CELL ANTIGEN.
REMOVED IN MATURE FORM (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         J-ANCHOR (POTENTIAL).
3FC1271742D657FA CRC64;
                                                            Score 645; DB 1;
Pred. No. 1.2e-58;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-PEB-2003 (Rel. 41, Last annotation update)
Prostate stem cell antigen precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 AA
                                                                                                                                                                                                                                       POTENTIAL.
EMBL; AF043498; AAC39607.1; -. EMBL; AJ297436; CAB97347.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12912 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               al Similarity 99.2
122; Conservative
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                                   Genew; HGNC:9500; PSCA
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                                                          MIM; 602470;
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Best Local
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PROPEP
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 VISKGCSLNCVDDSQDYYVGKKNITCCDTDLCNXSGAHALQPAAAILALLPALGLLLWGP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLT
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 41, Last annotation update)
19-PEB-2003 (Rel. 41, Last annotation update)
19-PEB-2003 (Rel. 41, Last annotation update)
19-PEB-2003 (Rel. 40-2)
19-PEB-2003 (Rel. 40-2)
19-PEB-2003 (Stem cell antigen 2) (SCA-2).
19-PEB-2003 (Stem Cellicken)
19-PEB-2003 (Chicken)
19-PEB-2003 (Chicken)
19-PEB-2003 (Chicken)
19-PEB-2003 (Passianidae; Passianidae; Passianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                 IN MATURE FORM (BY SIMILARITY).
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Petrenko O., Ischenko I., Enrietto P.J.;
Forracterization of changes in gene expression associated with
malignant transformation by the NF-kappaB family member, v-Rel.";
Oncogene 15:1671-1680(1997).
                                                                                                                                                                                                                                                                                                      UPAR/LY6.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . . ) (POTENTIAL).

N-LINKED (GLCNAC. . . . )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.1%; Score 388; DB 1; Length 123.
58.5%; Pred. No. 1.4e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC, ,) (POTE GPI-ANCHOR (BY SIMILARITY). CDA8566F37307ECC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35; Indels
                                                                                                  Probom; PD00312c, -, -, SMART; SM00134; LU; 1. -
PROSITE; PS00983; LY6 UPAR; 1. -
Antigen; Glycoprotein; Membrane; GFI-anchor; Signal. -
SIGNAL BY SIMILARITY. -
21 95 PROSTATE STEM CELL, ANTIGEN. -
123 REWOVED IN MATURE FORM (BY
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-!- TISSUE SPECIFICITY: EXPRESSED BY THYMIC BLAST CELLS.
-!- SIMILARITY: Contains 1 UPAR/Ly6 domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 AA.
                 InterPro; IPR003632; Ly-6 CD59.
InterPro; IPR001526; Ly-6 UPAR.
Pfam; PF00021; UPAR_LY6; 1.
ProDom; P0003128; Ly-6 CD59; 1.
SMART; SM00134; LU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13443 MW;
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nes 72; Conservative
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MGD; MGI:1919623;
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NCBI_TaxID=9031;
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SEQUENCE
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SEQUENCE
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                                                                                                                                                                                                                                                                                                  1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGL-- 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain, and Breast;
MEDLINE=96338158; PubMed=8757598;
Capone M.C., Gorman D.M., Ching E.P., Zlotnik A.;
"Identification through bioinformatics of cDNAs encoding human thymic shared Ag-1/stem cell Ag-2. A new member of the human Ly-6 family.";
J. Immunol. 157:969-973(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Lymphocyre antigen Ly-6E precursor precursor acid-induced gene E
Drotein) (RIG-E) (Thymic shared antigen-1) (RS4-1) (Stem cell antigen
                                                                                                      LYMPHOCYTE ANTIGEN LY-6E.
REMOVED IN MATURE FORM (BY SIMILARITY).
UPAR/LY6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUB-Promyelocytic leukemia;
MEDLINE=96234063; PubMed=8650192;
Mao M., Yu M., Tong J.-H., Ye J., Zhu J., Huang Q.-H., Fu G., Yu L.,
Zhao S.-Y., Waxman S., Lanotte M., Wang Z.-Y., Tan J.-Z., Chan S.-J.
Chen Z.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "RIG-E, a human homolog of the murine Ly-6 family, is induced by retinioc acid during the differentiation of acute promyelocytic leukemia cell.";
Proc. Natl. Aced. Sci. U.S.A. 93:5910-5914(1996).
                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POTENTIAL)
GPI-ANCHOR (POTENTIAL).
EB5C89E6674C73B8 CRC64;
                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                          DB 1; Length 126;
                                                                                                                                                                                                                                                               48; Indels
                                                                       PROSITE: PS00983; LY6 UPAR; FALSE NEG.
Signal; Antigen; Multīgene family; Membrane; GPI-anchor.
SIGNAL 1 20 POTENTIAL.
                                                                                                                                                                                                                                          Score 172.5; DB 1
Pred. No. 9.9e-11;
                                                                                                                                       BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNA
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          EMBL, L34554; AAA49063.1; -.
InterPro; IPR003632; Ly-6 CD59.
InterPro; IPR001526; LY6 UPAR.
Pfam; PF00021; UPAR_LY6; 1.
Probom; PD003128; Ly-6 CD59; 1.
SMART; SM00134; LU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq
28-FEB-2003 (Rel. 41, Last anno
                                                                                                                                                                                                                     13011 MW;
                                                                                                                                                                                                                                          26.7%;
35.5%;
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                                                                                                                                                                                                                    126 AA;
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Best Local Similarity
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016553;
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                                                                                                                                                                                                                 J. Immunol. 160:197-208 (1998).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRA-VGLL

    similarity).
    TISSUE SPECIFICITY: WIDELY EXPRESSED, PREDOMINATLY IN LIVER,
    TISSUE SPECIFICITY: WIDELY EXPRESSED, PREDOMINATLY IN LIVER,
    INDUCTION: BY RETINOIC ACID; IN PROMYELOCYTIC LEUKEMIA NB4 AND IN MYELOBLAST HL-60 CELL LINES, ACTIVATED BY INF-ALPHA IN MONOCYTIC CELL LINE U-937 AND IN PERIPHERAL BLOOD MONOCYTE CELLS.
    SIMILARITY: Contains 1 UPAR/Ly6 domain.

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REMOVED IN MATURE FORM (POTENTIAL).
UPAR/LYG.
BY SIMILARITY.
GOULDARY.
BY SIMILARITY.
GOULDARY.
BY SIMILARITY.
                                                                                                                                                     mouse
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                                                        Shan X., Bourdeau A., Rhoton A., Wells D.E., Cohen E.H., Landgraf B.E., Palfree R.G.E., "Characterization and mapping to human chromosome \thetaq24.3 Ly-6-related gene 9804 encoding an apparent homologue of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Signal; Antigen; MultIgene family; Membrane; GPI-anchor.
SIGNAL 1 20 POTENTIAL.
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24.5%; Score 158.5; DB 1
Best Local Similarity 35.3%; Pred. No. 2.7e-09;
Matches 47; Conservative 18; Mismatches 53
TISSUE=Monocytes;
MEDLINE=98211698; PubMed=9551972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 35
41 71
71 92
99 N
101 GF
13507 MW; C
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ProDom; PD003128; LY-6_CD59; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U42376; AAC50519.1; -. EMBL; U56145; AAC50616.1; -. EMBL; U66711; AAB07513.1; -. EMBL; Z68179; CAA92321.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 ALLPALGLLLWGP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 SLLPA--LLRFGP 131
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131
101
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PROSITE; PS00983; L)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Classon B.J., Coverdale L.;
"Genomic organization and expression of mouse thymic shared antigen-1
"Genomic organization and expression of mouse thymic shared antigen-1
(TSA-1): evidence for a processed pseudogene.";
Immunogenetics 44:22-226(1996).
-!- FUNCTION: INVOLVED IN T-CELL DEVELOPMENT.
-!- FUNCTION: INVOLVED IN ATLACHED to the membrane by a GPI-anchor.
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
-!- SIMILARITY: Contains 1 UPAR/Ly6 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Thymus;
MEDLINE=94261572; PubMed=8202484;
Classon B.J., Coverdale L.;
"Mouse stem cell antigen Sca-2 is a member of the Ly-6 family of cell surface proteins.";
Proc. Natl. Acad. Sci. U.S.A. 91:5296-5300(1994).
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               064253; Q61128;
15-UUL-1998 (Rel. 36, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Lymphocyte antigen Ly-6E precursor (Thymic shared antigen-1) (TSA-1)
(Stem cell antigen 2).
LYGE OR LYG 7 OR SCA-2-OR TSA-1.
                                                                                                                                                                                                                                                                                                                   Macnell I., Kennedy J., Godfrey D.I., Jenkins N.A., Masciantonio M., Mineo C., Gilbert D.J., Copeland N.G., Boyd R.L., Zlotnik A.; "Isolation of a cDNA encoding thymic shared antigen-1. A new member of the Ly6 family with a possible role in T cell development."; J. Immunol. 151:6913-6923(1993).
                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
130 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LY6_UPAR; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U09192; AAB03366.1; ALT_INIT.
EMBL; U04268; AAA19121.1; ALT_INIT.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=129/SvJ;
MEDLINE=96270003; PubMed=8662090;
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=94081342; PubMed=8258699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR0013632; Ly-6_CD59.
InterPro; IPR001526; Ly-6_UPAR.
Pffam; PF00021; UPAR. LY6; 1.
ProDom; PD003128; Ly-6_CD59; 1.
SMART; SM00134; LU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U47737; AAB17698.1; -.
STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                  NCBI_TaxID=10090;
MOUSE
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                                                                                                                                                                                                                                                                      61 NLGYTLNKGCSPICPSENVNLNLGVASVNSYCCQSSFCNFSAAGLGLRASIPLLGLGLLL 120
                                                                                                                                                                                                                                  57 GLLTVISKGCSLNCVDDSQDYYVGKKNIT--CCDTDLCNXS----GAHALQPAAILALL 110
                                                                                                                                                   1 MKAVILALIMAGIALOPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRA----V
                                                            10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=BALB/c; TISSUE=Leukocyte;
MEDLINE=95569850; PubMed=7642235;
Gumley T.P., McKenzie I.F., Sandrin M.S.;
Guglence and structure of the mouse ThB gene.";
Immunogenetics 42:221-224(1995).
-!- SUBCELLUAR LOCATION: Attached to the membrane by a GPI-anchor.
-!- TISSUE SPECIFICITY: TYMOCYTES AND B CELLS.
-!- SIMILARITY: Contains 1 UPAR/Ly6 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell antigen) (ThB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
LYMPHOCYTE ANTIGEN LY-6D.
REMOVED IN MATURE FORM (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Thymocytes;
MEDLINE=93017863; PubMed=1401899;
Gumley T.P., McKenzie I.F., Kozak C.A., Sandrin M.S.;
Isolation and characterization of cDNA clones for the mouse
22.3%; Score 144; DB 1; Length 130; 30.8%; Pred. No. 7.9e-08; ive 20; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE, PS00983; LY6 UPAR; 1.
Signal; Antigen; Multigene family; Membrane; GPI-anchor.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2010 (Rel. 40, Last annotation update)
LYGD OR THB OR LY61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY
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EMBL; L40419; AAA79249.1; ALT_INIT.
PIR; A46528; A46528.
MGD; MGI: 96881; Ly6d.
InterPro; IPR001362; Ly6 UPAR.
Pfam; PF00021; UPR01526; Ly6 UPAR.
ProDom; PF00031, UPAR.
ProDom; PF0003128; Ly6 CD59; I.
SMART; SM00134; LU; I.
                           30.8%;
                                                            40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                       111 PALGLLLWGP 120
                                                                                                                                                                                                                                                                                                                                                                                                             121 SLLALLQLSP 130
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   Query Match
Best Local Similarity
Matches 40; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOUSE
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DISULFID
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PROPEP
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60 -TVISKGCSLNCVDD-SQDYYV--GKKNITCCDTDLCN----XSGAHALQPA----AA 105
                                                                                                                                                                                                                                                               56 GNLVRKECANSCTSDYSQQGHVSSGSEVTQCCQTDLCNERLVSAAPGHALLSSVTLGLAT 115
                                                                                                                                                                                         1 KTALLVLLVLAVATSPAWALRCHVC---TNSANCKNPQVCPSNFYFCKT---VTSVEPLN 55
                                                                                                                                                                                                                                                                                                                                                                                  STANDARD; PRT; 103 AA.

SSUR HUMAN STANDARD; PRT; 103 AA.

PSSGOO, 092483;
01-OCT-1996 (Rel. 34, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Secreted Ly-6/uPAR related protein 1 precursor (SLURP-1) (ARS component B) (ARS (Component B) -81/S) (Anti-neoplastic urinary protein)
(ANUP).
                                                                                                                                                                      1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ridge R.J., Sloane N.H., "Partial N-terminal amino acid sequence of the anti-neoplastic urinary protein (ANUP) and the anti-tumour effect of the N-terminal nonapeptide of the unique cytokine present in human granulocytes."; Cytokine 8:1-5(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARTIAL SEQUENCE.
MEDIATRE-9922809; Lubwed=10211827;
Andermann K., Wattler F., Wattler S., Heine G., Meyer M.,
Forsemann W.-G., Nehls M.;
"Structural and phylogenetic characterization of human SLURP-1, the first secreted mammalian member of the Ly-6/upAR protein superfamily.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fischer J., Bouadjar B., Heilig R., Huber M., Lefevre C., Jobard Macari F., Bakija-Konsuo A., Ait-Belkacem F., Weissenbach J., Lathrop M., Hohl D., Prud'homme J.-F.;
"Mutations in the gene encoding SURP-1 in Mal de Meleda.";
Hum. Mol. Genet. 10:875-880(2001).
                                                                                                                                         20;
                                                                                                           19.5%; Score 126; DB 1; Length 127; 31.8%; Pred. No. 5.1e-06;
                                                                                                                                       51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mastrangeli R.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
                                                                           0AF039B77D105917 CRC64;
BY SIMILARITY.
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GPI-ANCHOR (POTENTIAL).
                                                                                                                         Pred. No. 5.16
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SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Granulocyte;
MEDLINE=96351837; PubMed=8742060;
                                                                            13395 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein Sci. 8:810-819(1999).
                                                                                                                         llarity 31.8%;
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   26
38
67
87
98
127 AA;
                                                                                                                         Similarity 42; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FISSUE=Placenta;
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                                                               LIPID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISEASE: Defects in SLURP1 are a cause of Mal de Meleda (MDM), a rare autosomal recessive skin disorder, characterized by transgressive palmoplantar keratoderma (PPK), keratotic skin lesions, perioral erythema, brachyddactyly and nail abnormalities. SIMILARLTY: Contains I UPAR/Ly6 domain.

CAUTION: IT IS NOT CERTAIN THAT ARS AND ANUP ARE IDENTICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECRETED LY-6/UPAR RELATED PROTEIN 1. UPAR/LY6.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miwa J.M., Ibanez-Tallon I., Crabtree G.W., Sanchez R., Sali A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.8%; Score 121.5; DB 1; Length 103;
TISSUE SPECIFICITY: GRANULOCYTES. EXPRESSED IN SKIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07AAF6BCA8031282 CRC64;
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POTENTIAL.
POTENTIAL.
A -> Q (IN REF. 2).
S -> A (IN REF. 2).
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18-FEB-2003 (Rel. 41, Last sequence update)
18-FEB-2003 (Rel. 42, Last annotation update)
Ly-6/neurotoxin-like protein 1 precursor (GC26)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .2e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005125; F:cytckine activity; NAS.
InterPro; IPR0013632; Ly-6 CD59.
InterPro; IPR001526; Ly6 UPAR.
Pfam; PF00021; UPAR LY6; 1.
ProDom; PD003128; Ly-6 CD59; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
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STRAIN=CS7BL/6; TISSUE=Cerebellum;
MEDLINE=99328647; PubMed=10402197;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A59031; A59031
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(Potential)

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Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alaxawa T., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kaaukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Ruchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Ano H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchioni L., Mashima J., Mondone P., Ring B., Ringwald M., Rodiguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Waller M., Weitz K., Wanji H., Kohtsuki S., Marcional annoteation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A REDLINE=22388257; PubMed=12477932;
A Strausberg R.L. Feingold E.A. Grouse L.H., Derge J.G.,
A Altschul S.F., Zeeberg B., Butcow K.H., Schaefer C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Butcow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Butcow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
A stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.B., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muxin D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Halton E., Retteman M., Madan A., Rodrigues S., Sanchez A.,
Butcaffield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Mara M.A.;
Human and mouse cDNA sequences.", Jones than 15,000 full-length
                        "Lynx1, an endogenous toxin-like modulator of nicotinic acetylcholine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuron 33:893-903(2002).
-!- FUNCTION: Seems to modulate nicotinic acetylcholine receptors.
Promotes the largest of three current amplitudes elicited by ACh through alpha (4) beta (2) nAChRs and that LYNXI enhances
                                                                                                                                                                        .;
the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ibanez-Tallon I., Miwa J.M., Wang H.L., Adams N.C., Crabtree G.W., Sine S.M., Heintz N.; "Novel modulation of neuronal nicotinic acetylcholine receptors by association with the endogenous prototoxin lynxl.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: Binds directly to nAChRs. SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
                                                                                                                                                                Miwa J.M., Fletcher C.F., Copeland N.G., Jenkins N.A., Heintz N. "Genetic mapping and characterization of Lynx1: a new member of
                                                                                                                                                                                                                                        Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUE=Hippocampus;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21904935; PubMed=11906696;
                                               the mammalian CNS.";
                                                                                                                                                                                                                    /neurotoxin superfamily.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 409:685-690(2001).
                                                                     Neuron 23:105-114(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 KVRKSCVPSCFETVYDGYSKHASATSCCQYYLCNGAGF----ATPVTLALVPALLATFW 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99017973; PubMed=9799603;
Horie M., Oktucmi K., Taniguchi Y., Ohbuchi Y., Suzuki M.,
Takahashi E.-I.;
"Isolation and characterization of a new member of the human Ly6 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 VISKGCSLNCVDDSQDYXVGKKNIT-CCDTDLCNXSGAHALQPAAAILALLPALGLLLW
           TISSUE SPECIFICITY: Expressed in brain. Expressed in neurons in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                  LY-6/NEUROTOXIN-LIKE PROTEIN 1.
REMOVED IN MATURE FORM (POTENTIAL).
UPAR/LY6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
GPI-ANCHOR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.9%; Score 115.5; DB 1
27.7%; Pred. No. 5.5e-05;
tive 15; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 AA.
                          multiple brain structures.
-!- SIMILARITY: Contains 1 UPAR/Ly6 domain.
                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lymphocyte antigen Ly-6H precursor
                                                                                                                                                                                                                                                                                   Pfam, PF00021; UPAR LY6; 1.
ProDom; PD003128; Ly-6 CD59; 1.
SMART; SM00134; LU; 1.
                                                                                                                                                                                                                                                       InterPro; IPR003632; Ly-6_CD59.
InterPro; IPR001526; LY6_UPAR.
                                                                                                                                                                                   EMBL; AF141377; AAD38939.1; -. EMBL; AF169202; AAF16899.1; -.
                                                                                                                                                                                                             EMBL; AK013827; BAB29006.1; -. EMBL; BC037541; AAH37541.1; -. MGD; MGI:1345180; Lynx1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12835 MW;
                                                                                                                                                                                                                                                                                                                            Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 27.7%
les 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomics 53:365-368(1998)
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                                                                                                                                                                                                                                                                                                                                           20
1116
101
107
103
64
85
93
                                                                                                                                                                                                                                                                                                                            3PI-anchor; Membrane;
SIGNAL 1 20
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                                                                                                                                                                                                                                                                                                                                                                                                                           39
68
86
93
116 AA;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LY6H_HUMAN
094772;
                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
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126 AA; 14066 MW;
                                                                          105 AILALLPALG-LLLW-GP
                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 TSLAGLGLW 123
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70
                                                                                                                                                                                                                                                                                                                                                                                                         LYGGEC OR NG24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=129;
                                                                                                                                                                                                                                          MOUSE
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LY6H_MOUSE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                  A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Straubberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Whiting M., Touchman J.W., Schevrenko Y., Bouffard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
B Blakesley R.W., Touchman J.W., Sralska U., Shailus D.E.,
A Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length
Human and mouse colby & etgeners."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WKGLGLALLAVLLCSAPAHGLWCQDCTLTTNSSHCTP-KQCQPSDTVCASVRITDPSSSR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMYGDALA, HIPPOCAMPUS AND SUBTHALAMIC NUCLEUS) AND IN ACUTE HUMAN LEUKEMIC CELL LINE MOLT-3. ALSO FOUND IN LOWER LEVELS IN TESTIS, PANCREAS, SMALL INTESTINE AND COLON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: Contains 1 UPAR/Ly6 domain. CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN (CEREBRAL CORTEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00983; LYG_UPAR; FALSE_NEG.
Signal; Antigen; Multigene family; Membrane; GPI-anchor.
Signal
1 25 POTENTIAL
1 25 LYMPHOCYTE ANTIGEN LY-6H.
CHAIN
PROPEP 116 140 REMOVED IN MATURE FORM (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .) (POTENTIAL)
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A9274BFE89B6CBA3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Pred. No. 8.2e-05; 15; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GLCNAC.
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GO; 600:007397; P.histogenesis and o:
GO; GO:0007399; P.neurogenesis; TAS.
InterPro; IPR001526; LY6_UPAR.
                        PubMed=12477932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB012293; BAA34115.1; -. EMBL; BC028894; AAH28894.1; -. EMBL; BC030192; AAH30192.1; -.
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SMART; SM00134; LU; 1.
PROSITE; PS00983; LY6_UPAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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nes 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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MIM; 60
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61 ---VISKGCSLNCVDD-----SQDYYVG------KKNITCCDTDLCNXSGAHALQPAA 104

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between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
65 KDHSVNKMCASSC--DFVKRHFFSDYLMGFINSGILKVDVDCCEKDLCNGAAGAGHSPWA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 TVISKGCSLNC------VDDSQDYYVG-KKNITCCDTDLCNXSGAHALQPAAAILAL 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Lymphocyte antigen 6 complex locus G6C protein precursor (Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
LYMPHOCYTE ANTIGEN 6 COMPLEX LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rowen L., Madan A., Qin S., Shaffer T., Ratcliffe A., Abbasi N. Dickhoff R., James R., Loretz C., Lasky S., Hood L.; "Sequence of the mouse major histocompatibility locus class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 17.3%; Score 111.5; DB 1; Similarity 31.8%; Pred. No. 0.00015; 41; Conservative 19; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Secreted (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                             126 AA.
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                                                                                                                                      || :|| ||| ||
123 LAGGLLLSLGPALLWAGP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF109905; AAC84157:1; -. MGD; MGI:2148930; Ly6g6c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001
16-OCT-2001
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 TVISKGCSLNC---VDDSQDYY--VGKK----NITCCDTDLCNXSGAHALQPAAAILAL 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 WVFS---NLRCGTPEEPCQEAFNQTNRKLGLTYNTTCCNKDNCNSAGPRP-TPALGLVFL 113
                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=22074936; PubMed=12079290;
MAILYA M., Campbell R.D., Aguado B.;
"Transcriptional analysis of a novel cluster of LY-6 family members in "Transcriptional analysis of a novel the thuman and mouse major histocompatibility complex: five genes with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENC-TQLGEQCWTARIRAVGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shiina S., Tamiya G., Oka A., Inoko H.;
"Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
Submitted (SEP-1999) to the EMBL/Genbank/DDBJ databases.
-i- SUBCELLULAR LOCATION: Secreted (Potential).
-i- SIMILARITY: SOME, TO LY-6/UPAR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYMPHOCYTE ANTIGEN 6 COMPLEX LOCUS G6C PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                  Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A., Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J., Lasky S., Hood L.; "Sequence of the human major histocompatibility complex class III
28-FEB-2003 (Rel. 41, Last annotation update)
Lymphocyte antigen 6 complex locus G6C protein precursor (Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.6%; Score 101; DB 1; Length 125; 29.5%; Pred. No. 0.0017; tive 23; Mismatches 50; Indels
                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutel
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 AA; 13821 MW; 9ED7549894C71311 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         · POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ315533; CAC85539.1; -. EMBL; AF129756; AAD18076.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLUR_MOUSE STANDARD;
1D SLUR MOUSE STANDARD;
AC 0920R7;
DT 16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AP000504; BAB63379.1;
Genew, HGNC:13936; LY6G6C.
SMART; SMO0134; LU; 1.
                                                                                                                                                                                                                                                                                                                                        Genomics 80:113-123(2002).
                                                              LYGGGC OR NG24 OR C6ORF24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 LPALGLLLW 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 TSLAGLGLW 122
                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                     forms
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                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF129756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    region."
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 KDHSVNKMCASSC--DFVKRHFFSDYLMGFINSGILKVDVDCCEKDLCNGASVAGRSPWA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---VISKGCSLNCVDD-----SQDYYVG-----KKNITCCDTDLCNXSGAHALQPAA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 MKSLGLALLALLLCPSPAHGLWCODC - TLANSSHCAPKQCQPTDTVCASVRITDPSSSR
                                                                                                                                                                                                                                 Apostolopoulos J., Chisholm L.J., Sandrin M.S.; in normal tissue."; "identification of mouse Ly6H and its expression in normal tissue."; Immunogenetics 49:997-990(1999).
--- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: Contains 1 UPAR/Ly6 domain.
CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-6 IS THE INITIATOR.
                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: STRONGLY EXPRESSED IN BRAIN, ALSO FOUND LOWER LEVELS IN EYE AND REPRODUCTIVE TISSUES.
DEVELOPMENTAL STAGE: EXPRESSION INCREASES DURING EMBRYONIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal; PRO0983; LY6 UPAR; FALSE NEG.
Signal; Antigen; MultIgene family; Membrane; GPI-anchor.
SIGNAL
1 25 POTENTIAL.
CHAIN 26 110 LYMPHOCYTE ANTIGEN LY-6H.
PROPEP 111 339 REMOVED IN MATURE FORM (POTENTIAL).
DOMAIN 26 113 UPAR/LY6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.2%; Score 111; DB 1; Length 13:
29.7%; Pred. No. 0.00019;
.ive 16; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FDEEC13591EF219C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
N-LINKED (GLCKNC...)
GPI-ANCHOR (POTENTIAL).
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(Rel. 40, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF127091; AAD28600.1; ALT_INIT.
MGD; MGI:1346030; Ly6h.
InterPro; IPR001526; LY6 UPAR.
PFam: PF00021; UPAR_LY6; 1.
         Lymphocyte antigen Ly-6H precursor.
                                                                                                                                                                                STRAIN=BALB/c; TISSUE=Brain;
MEDLINE=99432011; PubMed=10501842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAGGLLLSLGPALLWAGP 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 AILALLPALG-LLLW-GP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 29.77
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 AA;
                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            similarity).
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16-OCT-2001
16-OCT-2001
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SEQUENCE
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16-OCT-2001 (Rel. 40, Last sequence update)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TROM N.A.

SEQUENCE TROM N.A.

MEDINE-21085660; Dubmed-11217851;

MEDINE-21085660; Dubmed-11217851;

Arakawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Alzawa T., Izawa M., Nishii K., Kiyosawa H., Koaukawa T., Samanaka I.,

Balato T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda T., Gissi C., King B., Kochiwa H.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suutki R., Tomita M., Wagner L., Washing N.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Flercher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Monbaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayashizaki Y.,

Natura Ang. Ang. Ang. Ang. Ang. Lall-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                               STRAIN-BALB/c;
Mastrangeli R., Donini S., Kelton C., Lou S., Serlupi-Crescenzi O.,
Vaccaro R., Renda T., Bressan A., Micangeli E., Milazzo F., Ciolli V.,
Biffoni M., El Tayar N., Lisciani R., Borrelli F., Martelli F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECRETED LY-6/UPAR RELATED PROTEIN 1.
                                                                                                                                                      Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serani S., Papoian R.; "Cloning of ARS gene, Component B, a new member of Ly-6-related
                                  28-FEB-2003 (Rel. 41, Last annotation update)
Secreted Ly-6/uPAR related protein 1 precursor (SLURP-1) (ARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
AAB69CF6C5FE5BFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 400:685-690(2001).
-1- SUBUNIT: Homodimer (By similarity).
-1- SUBCELLULAR LOCATION: Secreted (By similarity).
-1- SIMILARITY: Contains 1 UPAR/Ly6 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
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InterPro; IPR001526; LY6_UPAR.
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110
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99
12016 MW,
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EMBL; AK003904; BAB23068.1; -.
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                                                                                            component B)
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                                                                                                                                  61
                                                                                                                                                                          10 LILAAWSMGYGBAFRCYTCEQPTAINSCKNIAQCKMEDTACKTV-----LETVEAAFPF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gong N.L., Armugam A., Jeyaseelan K.;
"Molecular cloning, characterization and evolution of the genes
encoding a new group of short-chain alpha-neurotoxins in an Australian
elapid, Pseudonaja textilis.";
FEBS Lett. 473:303-310(2000).
-!- FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic
acetylcholine receptors (nACAR) (By similarity).
-!- SUBCELULIAR LOCATION: Secreted (By similarity).
-!- TISSUE SPECIFICITY: Expressed by the venom gland (Probable).
-!- SIMILARITY: Belongs to the snake toxin family.
                                                                                                                                  8 LLMAGLALOPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLTV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gong N.L., Armugam A., Jeyaseelan K.; "Poetsynaptic short-chain neurotoxins from Pseudonaja textilis: cDNA cloning, expression and protein characterization."; Eur. J. Biochem. 265:982-989(1999).
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudonaja textilis (Eastern brown snake).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Acanthophiinae; Pseudonaja.
                                                                  17;
ch 15.4%; Score 99.5; DB 1; Length 110; 1 Similarity 25.8%; Pred. No. 0.0022; 25; Conservative 13; Mismatches 42; Indels 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probom; Provocy, communication of the problem; Probom; Prostor; Probom; Prostor; Probom; Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Short neurotoxin 6 precursor (Alpha neurotoxin 6).
                                                                                                                                                                                                                                                                                                                          64 NHSPMVTRSCSSSCLATDPDGIGVAHPVFCCFRDLCN 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND IDENTIFICATION OF INTRONS
                                                                                                                                                                                                                                                              ----ISKGCSLNCVDDSQDYYVGKKNITCCDTDLCN 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-Venom gland;
MEDLINE=99449602; PubMed=10518793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Venom gland;
MEDLINE=20279909; PubMed=10818230;
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Pfam; PF00087; toxin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
      Query Match
Best Local Similarity
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NXS6_PSETE
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Matches
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                                                                                                                                                                                        1 MKAVLLALLMAG-LALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fodor W.L., Rollins S.A., Blanco-Caron S., Burton W.V.,
Guilmette E.R., Rother R.P., Zavoico G.B., Squinto S.P.;
Frinate terminal complement inhibitor homologues of human CD59.";
Immunogenetics 41:51-51(1995).
I- FUNCTION: POTENT INHIBITOR OF THE COMPLEMENT MEMBRANE ATTACK
COMPLEX (MAC) ACTION. ACTS AT OR AFTER THE C5B-8 STAGE OF MAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
CD59 glycoprotein precursor (Membrane attack complex inhibition factor) (MACIF) (MAC-inhibitory protein) (MAC-IP) (Protectin).
                                                                                                                                     17;
                                                                                  DB 1; Length 79;
                                                                                                                                     39; Indels
BY SIMILARITY.
73676636A59E947D CRC64;
                                                                                                                                                                                                                                                                                                                                            AIIDRGCSTSC-----PGGNRPVCCSTDLCN 78
                                                                                                                                                                                                                                                                                                    60 TVISKGCSLNCVDDSQDYYVGKKNITCCDTDLCN 93
                                                                                                      0.0032;
                                                                               Score 96.5; DB
Pred. No. 0.003
8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).
-!- SIMILARITY: Contains 1 UPAR/Ly6 domain.
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InterPro, IPRO01526, Ly6 UPAR.
Pfam, PF00021, UPAR. LX6, 1.
ProDom, PD003128, Ly-6 CD59, 1.
SMART; SM00134, LU; 1.
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ilarity 31.9%;
Conservative
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                            8570 MW;
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HSSP; P13987; 1CDS.
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  72
79 AA;
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                                                                                                                                 7 SVLFGLLLALAVFCHSGHSLQCYNCPNPTTN--CKTAINCSSGFDTCLIARAGLQVYNQC
                                                                        41; Gaps
                                           DB 1; Length 126;
                              14.9%; Score 96.5; DB 1; Lengua 25.0%; Pred. No. 0.005; Wiemarches 42; Indels
                                                                                                    3 AVLLALLMA-GLALQPGTALLCYSCKAQVSNEDCLQVENCT-----
GPI-ANCHOR (BY SIMILARITY)
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             13716 MW;
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126 AA;
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Best Local Similarity
Matches 33; Conserv
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August 18, 2003, 19:38:29 ; Search time 96 Seconds (without alignments) 330.630 Million cell updates/sec

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646 1 MKAVLLALLMAGLALQPGTA......AAILALLPALGLLLWGPGQL 123 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

830525 segs, 258052604 residues Searched:

830525 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL .. Database

Bp_invertebrate:*
Bp_mammal:* sp_organelle:* sp_phage:* sp_archea:* sp_bacteria:* sp_fungi:* sp_human:* ap_mhc: *

unclassified:* sp_vertebrate:* sp_rvirus:*
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sp_plant: *
sp_rodent: *
sp_virus: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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9	122			4	O81V16	Ogivie homo sapien
7	117.5			4	Q96AC2	O96ac2 homo sapien
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11	111			11	Q8K356	O8k356 mus musculu
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ALIGNMENTS

KRY SACUENCE KYON N. A.

SKANIECS7BL/GS. TISSUE-Stomach;

RX KAWAIN-CS7BL/GS. TISSUE-Stomach;

RX KAWAI J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Azawa K., Izawa M., Nishi K., Siyosawa H., Kondo S., Yamanaka I.,

RA Azawa K., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Fleischmann W., Gasterland T., Gissi C., King B., Kochiwa H.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barah G.,

RA Bake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Bake J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerte P.,

RA Sacaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Milming L.,

RA Hayashizaki Y.,

RA Hayashizaki Y., Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 01-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUAR-2003 (TrEMBLrel. 23, Last annotation update) 2210408804Rik protein (Prostate stem cell antigen). PSCA OR 2210408B04RIK. 123 AA. PRT; PRELIMINARY; Mus musculus (Mouse) [1] SEQUENCE FROM N.A. NCBI_TaxID=10090; Q9D7U0 007060

"Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001). [2] SEQUENCE FROM N.A.

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Pfam; PF00021; UPAR_LY6; 1.
ProDom; PD003128; LY-6_CD59; 1.
SMART; SM00134; LU; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003632; Ly-6 CD59.
InterPro; IPR001526; LY-6 UPAR.
Pfam; PF00021; UPAR_LY6; 1.
ProDom; P0003128; Ly-6_CD59; 1.
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HSSP; P13987; 1ERG.
                                                                                                                                                                        40; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                111 PALGLLLWGP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 SLLALLQLSP 136
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0610005K03RIK.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VISKGCSSQCEDDSENYYLGKKNITCCYSDLCNVNGAHTLKPPTTLGLLTVLCSLLLMGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKTVFFLLLATYLALHPGAALQCYSCTAQMNNRDCLNVQNCSLDQHSCFTSRIRAIGLVT 60
                                              Yang D., Holt G.E., Velders M.P., Kwon E.D., Kast W.M.;
"Muxine six-transmembrane epithelial antigen of the prostate, prostate specific mentigen, and prostate-specific membrane antigen; prostate-specific cell-surface antigens highly expressed in prostate cancer of transgenic adenocarcinoma mouse prostate mice.";
Cancer Res. 61.8557-8560(2001).
EMBL; AK008851; BAB25929.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLT
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC005684; AAH05684.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00134; LU; 1. TPROSITE; PS00983; LY6 UPAR; 1. SEQUENCE 123 AA; 13477 MW; 67A8566F3D30797A CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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LY6E.
                             MEDLINE=21371909; PubMed=11479226;
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MGD; MGI:1919623; Psca.
InterPro; 1PR003632; Ly-6_CD59.
InterPro; 1PR001526; Ly6_UPAR.
Pfam; PF00021; UPAR_LY6; 1.
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InterPro; IPR001526; LY6_UPAR.
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Submitted (APR-2001)
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Submitted (JAN-2001)
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Submitted (FEB-2001)
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SX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arawawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Azawa K., Isawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsudi F., Saito R.,

Radota K., Matsudi F., Saito R.,

Radota K., Matsudi F., Suzuki R., Tomita M., Wagner L., Washio T.,

Romstein M.J., Bult C., Fletcher C., Fuljita M., Gariboldi M.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Hayashisaki Y.,
                                                                                                                                                                                                                                                                          1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRA----V 56
                                                                                                                                                                                                                                                                                                                            10; Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
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                                                                                       22.3%; Score 144; DB 11; Length 136; 30.8%; Pred. No. 5.1e-09; tive 20; Mismatches 60; Indels 10
136 AA; 14392 MW; SAICBBE1464DC029 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Q81V16
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                                                                                                       65 GDSTVTKSCASKCEPSDVDGIGQTRPVSCCNSDLCNVDGAPSLGSPGGLLLAL--ALFLL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CS7BL/6J; TISSUE=Embryo;

Kawai U., Shinagawa A., Shibbata K., Yoshino M., Itoh M., Ishii Y.,

Kawai U., Shinagawa A., Shibbata K., Konno H., Adachi J., Fukuda S.,

Azawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Kadota K., Matsuda H.A., Aglobori T., Gissi C., King B., Kochiwa H.,

A Kadota K., Matsuda H.A., Carabura M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Bake J., Sofielli D., Bojunga M., Carninci P., Geniboldi M.,

Burownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Custincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Chyons P., Marchionni &., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sazaki H., Toyo-oka K., Wang K., Mang K., Manittaker C., Wilming L.,

Suzuki H., Toyo-oka K., Wang K., Mang K., Manittaker C., Wilming L.,

Suzuki H., Toyo-oka K., Wang K., Manitt C., Wang K., Manitti H., Sazaki H., Sazaki H., Sazoki H.
4 VLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLL---- 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                          133 AA
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InterPro; IPR001526; LY6 UPAR.
Pfam; PF00021; UPAR_LY6; 1.
ProDom; PD003128; Ly-6_CD59; 1.
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Best Local Similarity 30.74
Matches 31, Conservative
                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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XINDINE-21085660; PubMed=11217851;

XINDINE-2108560; PubMed=11217851;

XINDINE-210860; PubMed=11217851;

XINDINE-210860; PubMed=11217851;

XINDINE-210860; PubMed=11217860;

XINDINE-210860;

XINDINE-210860
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                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae, Murinae; Mus.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 GCSLNCVDDSQDYYVGKKNITCCDTDLCNXSGAHALQPAAAILAL 109
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein (Fragment)
Homo sapiens (Human).
                                                                                                                    Last sequence update)
Last annotation update)
    111 AA.
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                                                                            Created)
PRT;
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InterPro; IRR003632; Ly-6 CD59.
InterPro; IPR001526; LY6 UPAR.
Pfam; PP00021; UPAR_LY6; I.
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    PRELIMINARY;
                                                                    01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 409:685-690(2001)
                                                                                                                                                                                        2010109103Rik protein.
2010109103RIK.
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                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
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nes 33; Conserv
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SEQUENCE FROM N.A.
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SEQUENCE
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                                                    Q8N2G4
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Matches
                        RESULT 8
Q8N2G4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 MYRKSCASSAACLIASAGYQSFCSPGKLNSVCISCCNTPLCNGPRPKKRGSSASALRPGL 125
                                                                                                                                                                                                                                       88 LRCYTCKSLPRDERCNLTQNCSH-GQTCTTLIAHGNTESGLLTTHSTWCTDSCQPITKTV 146
                                                                                                                                                                          31 AVLLALLICG---RPGRGQTQQEEEEEDBDHGPDDYDEEDEDEVEEEETNRLPGGRSRVL 87
                                                                                                                                                                                                             21 LLCYSCKAQVSNEDCLQVENCTQLGEOCWTARIRA---VGLLTVISKGCSLNCVDDSQDY 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 IAATFCGLFLLPGFALQIQCYQCEEFQLNNDCSSPEFIVNCTVNVQDMCQKEVMEQSAGI 65
                                                                                                                                                                                                                                                                 78 YVGKKNITCCDTDLCNX------SGAHALQPAAAILALPALGLL 116
                                                                                                                                                                                                                                                                                          147 EGTQVTMTCCQSSLCNVPPWQSSRVQDPTGKGAGGPRGSSETVGAALLLNLLAGLGAM 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kawakami B., Sugiyama A., Takemoto M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsaura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Wurakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; "NEDO human cDNA sequencing project."; "NEDO human cDNA sequencing project."; "Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC017318; AAH17318.1; "."
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                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                  68;
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                                                                                                       18.9%; Score 122; DB 4; Length 209; 24.2%; Pred. No. 3.1e-06; ive 18; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.2%; Score 117.5; DB 4; Length 32.8%; Pred. No. 6.9e-06; ive 13; Mismatches 54; Indels
                Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases. EMBL, BC035810; AAH35810.1; -- Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 protein.
141 AA; 15240 MW; CFA6D98BA90792E3 CRC64;
                                                                              209 AA; 22320 MW; 1F3A2B890CEA6724 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 19, Last sequence update) (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                             141 AA
                                                                                                                                                           3 AVLLALLMAGLALQPG-------
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                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein FLJ37182. Homo sapiens (Human).
                                                                                                                                 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IISSUE=Alzheimer cortex;
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                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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Matches 43; Conserv
                                                                                                                   Local Similarity
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               Strausberg R.;
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01-OCT-2002 (
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SEQUENCE
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Q96AC2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTVISKGCSLNCVDDSQDYY----VGKKN---ITCCDTDLCN-----XSGAHALOP 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CS7BL/6J; TISSUE=Brain; MEDINE=22354683; PubMed=12466851; The FANTOM CONSOrtium. The FANTOM Consortium. The FANTOM Consortium the RIKEN Genome Exploration Research Group Phase I & II Team; Analysis of the mouse transcriptome based on functional annotation of 60,70 full-length CDNAs."; Nature 420:563-573(2002).

EMBL; AK045592; BAG32428:1; -.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                           TISSUE-Ovarian carcinoma;
Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii. Cta T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y., Nagahari K., Sugano S., Isogai T.;
"HRI human cDNA sequencing project.";
Submitted (WAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO75487; BAC11647.1;
Hypothetical protein.
SEQUENCE 165 AA; 17900 MW; 2BOBBD68044C8999 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.3%; Score 111.5; DB 11; Length 31.6%; Pred. No. 3.5e-05; tive 14; Mismatches 56; Indels
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SEQUENCE 141 AA; 15261 MW; 51717F7922C02DAA CRC64;
                                                      Created)
Last sequence update)
Last annotation update)
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17.7%; Score 114.5; DB 4
Best Local Similarity 33.9%; Pred. No. 1.9e-05;
Matches 40; Conservative 13; Mismatches 44
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   165 AA.
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                                                   01-OCT-2002 (TrEMBLrel. 22, Created 01-OCT-2002 (TrEMBLrel. 22, Last se 01-OCT-2002 (TrEMBLrel. 22, Last an Hypotherical protein OVARC1001499. Homo sapiens (Human).
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Conservative 1
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
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nes 42; Conserv
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SEQUENCE
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neopera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 AA; 15055 MW; A32C221F07E0860F CRC64;
                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.2%; Score 111; DB 5;
27.3%; Pred. No. 4.1e-05;
iive 15; Mismatches 61;
                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly)
                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE003668; AAF53941.1;
                                                105 AILALLPALGLLL 117
                                                                                126 LTTLLFFHLALCL 138
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Matches 39; Conservative
                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      CG14401 protein. CG14401.
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61; Indels

-----QVSNEDCLQVENCTQLGEQ 47 28;

1 MKAVLLALLMAGLALQPGTALLCYSCKA----

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61 ATCLTKYHEGMPGDTRFVRRSCYFGDASPIGVSC-DDGPDPVVPFMNFLGCTLCDTDLCN 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---VISKGCSLNCVDD-----SQDYYVG-----KKNITCCDTDLCNXSGAHALQPAA 104
93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLT 60
                                                                 --CWTARIRAV-GLLTVISKGC-----SLNCVDDSQDYYVGKKNI----TCCDTDLCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Osada N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugano S., Hashimoto K.; "isolation of full-length cDNA clones from mouse brain cDNA library made by oliog-capping method."; "Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AB041649; BAA95101.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.2%; Score 111; DB 11; Length 160; 29.7%; Pred. No. 4.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.; Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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E 160 AA; 17028 MW; 01536076672DCD75 CRC64;
                                                                                                                                                                                                                                                                                                                                                            01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to lymphocyte antigen 6 complex, locus H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UJUN-2002 (TrEMBLrel. 21, Last annotation update)
Brain CNRA, clone WCCD-0671.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                    160 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 AA.
                                                                                                                                                         94 XSGAHALOPAAAILALLPALGLL 116
                                                                                                                                                                                                   120 AAAGLSTLPLVIALSILGLLVLL 142
                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         105 AILALLPALG-LLLW-GP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, BC028758; AAH28758.1; -.
InterPror; IRRO01826; LY6_UPAR.
Pfam; PF00021; UPAR_LY6; 1.
SMART; SM00134; LU; 1.
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Best Local Similarity 29.78
Matches 41; Conservative
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                                                                                                                                                                                                                                                                                             6 IAATFCGLFWLPGLALQIQCYQCEEFQLNNDCSSPEFIVNCTVNVQDMCQKEVTEQSAGI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Abdominal gland;
MEDLINE-99402961; PubMed=10471817;
MEDLINE-99402961; PubMed=10471817;
Iwata T., Umezawa K., Toyoda F., Takahashi N., Matsukawa H.,
Yamamoto K., Miura S., Hayaahi H., Kikuyama S.;
"Molecular cloning of newt sex pheromone precursor cDNAs: evidence for the existence of species-specific forms of pheromones.";
FEBS Lett. 457:400-404(1999).
EMBL, AJ245555; CAB53093.1; .
SEQUENCE 189 AA; 20461 MW; FO06C709F6F040AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cynops pyrrhogaster (Japanese common newt).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
NCBI_TaxID=8330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46;
                                                                                                                  17.1%; Score 110.5; DB 11; Length 141; 31.6%; Pred. No. 4.6e-05; cive 13; Mismatches 57; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.4%; Score 106; DB 13; Length 189; 26.6%; Pred. No. 0.00022; ive 18; Mismatches 38; Indels 46
                           SM00134; LU; 1.
SE 141 AA; 15231 MW; C8716DDC65228BED CRC64;
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Last annotation update)
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Last annotation update)
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CG6579.
Drosophila melanogaster (Fruit fly)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 VPPPDDTPSGCGSDQPCTA 127
   InterPro; IPR001526; LY6_UPAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 AILALLPALGLLL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 LTTLLFFHLALCL 138
                                                                                                                                                 Local Similarity 31.6
nes 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 26.6
Matches 37; Conservative
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                              SMART; SM
SEQUENCE
                                                                                                                     Query Match
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Search completed: August 18, 2003, 19:43:39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKAVLLALLMAGLALQPGTALLCYSCKA-----QVSNEDCLQVENCTQLGEQCWTA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
density lipoprotein binding protein
                                                                                                                                Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.0%; Score 103.5; DB 5; Length 185; 23.2%; Pred. No. 0.00041; ive 26; Mismatches 47; Indels 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 RIRAVGLL-----TVISKGCSLNCVDDSQDYYVGKKNITC----
                                                                                                                                                                                                                                                                                               FlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003635; AAF53179-2; --
FlyBase; FBGN0033422; CG6579.
SEQUENCE 185 AA; 20370 MW; BBECDAIAS5414BE2 CRC64;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ioka R.X., Kang M., Kim D., Fujino T., Yamamoto T.T.;
"High Density Lipoprotein Binding Protein 1.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TDLCNXSGA--HALOPAAAILALLPALGLLL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 AA.
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MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003 (TrEMBLrel. 23, 1110002J19Rik protein (High
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 23.2
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61 LOCYFCQVLHSGESCNOTOSCSSSKPFCITLVSHSGTDKGYLTTYSMWCTDTCQPIIKTV 120
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4 LRAVLLILLLSG---QPGSGWAQEDGDADPEPENYNYDDDDDEEEEEETNMIPGSRDRAP 60
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                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                   46;
                                                                                                                                                                                                                                                                                              15.9%; Score 103; DB 11; Length 228; 24.3%; Pred. No. 0.0006; ive 14; Mismatches 43; Indels 46
                                                                                                                                                                                                                                                 228 AA; 24566 MW; B2FB456A10865E81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  1 MKAVLLALLMAGLALQPGTA------
                                                                                                                                                                        PROSITE; PS00290; IG MHC; 1.
PROSITE; PS00983; LY6_UPAR; 1.
EMBL; AK003305; BAB22704.1; -.
                                                               InterPro, IPR003006; Ig MHC.
InterPro, IPR001526; LYG UPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTQMTQTCCQSTLCN 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 YVGKKNITCCDTDLCN 93
                                                                                                                      Pfam; PF00021; UPAR LY6; 1. SMART; SMO0134; LU; 1.
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 24.3%;
                                                                                                                                                                                                                          Lipoprotein.
SEQUENCE
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GenCore version 5.1.6
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                 Copyright
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- protein search, using sw model OM protein

Run on:

August 18, 2003, 19:38:54; Search time 39 Seconds (without alignments) 303.301 Million cell updates/sec

US-09-934-586A-2 646 score:

1 MKAVLLALLMAGLALQPGTA........AAILALLPALGLLLWGPGQL 123 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		٠			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
-	144	22.3	136	8	I49013	thymic shared anti
7	126	19.5	127		A46528	phosphatidylinosit
М	126	19.5	130	-	I54553	gene ThB protein -
4	_:		103		A59031	
S	100.5	15.6	135	N	A45835	homolog RK1(
9	ı.	14.9	126		136914	protein - ba
7	•	14.9	510		A42635	activin receptor S
60	96	14.9	368	-	T21748	hypothetical prote
σ	95	14.7	128		A57321	Q
10	95	14.7	222		B41643	urokinase-type pla
11	95	14.7	222		B55356	urokinase-type pla
12	95	14.7	327		A55356	
13	94.5	14.6	126		S53340	
14	94	14.6			B40829	activin receptor i
15	94	14.6	528		C40829	activin receptor i
16	93	14.4	83		S70374	cardiotoxin V prec
17		14.3	128		RWHU59	surface glycoprote
18	92.5	14.3	328		S42152	urinary plasminoge
19	92	14.2	134		D45835	Ly6 homolog RK3 pr
20		14.2	365		S27268	activin receptor S
21	91.5	14.2	510		A56926	activin receptor I
22	91	14.1	512		137134	activin type II re
23	90	13.9	246		B37225	acrosomal protein
24	06	13.9	512		D40829	activin receptor i
25	90	13.9	513		JQ1484	activin receptor p
56	90	13.9	536		A40829	
	89.5	13.9	285		177964	SP-10 - western ba
28	83	13.8	251	7	157999	Φ
53	88.5	13.7	265		A37225	acrosomal protein

BMP receptor precu venom protein C9S3	Dpp receptor SAX p CD59 protein - gre complement regulat	hypothetical prote cardiotoxin VII pr sporm acrosome ant miscariic foxin b	neurotoxin-like pe long neurotoxin l hypothetical prote hypothetical prote protein T22A3.8 [i
A54985 V6EP9A A37910	145712 136894 156894	113389 S70375 I52518	S19951 N2NJ1R T22167 T23064 F87908
210	10000	1000	
527 86 86	570 128 131	1291 1291 82 261 261	342 342 2823 2823
13.3	13.02	1225	11.9
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30	1 W W W V	0 K K K K 0 C B C C	, 4 4 4 4 4 5 4 5 6 4 6

ALIGNMENTS

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C,Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: 149013; 148910
C;Accession: 149013; 148910
C;Accession: 149013; 148910
C;Accession: 149013; 14991
C;Accession: 149013; MUID:94081342; PMID:8258699
C;Accession: 149013
thymic shared antigen-1 - mouse
N/Alternate names: Sca-2 precursor; TSA-1
C,Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                            A;Status: translated from GB/EMBL/DDBJ
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A; Molecule type: mRNA A; Mesaduces: 1.136 cRES, A; Cross-references: EMBL: U09192; NID:9487390; PIDN:AAB03366.1; PID:9487391 R; Classon, B.J.; Coverdale, L. R; Classon, B.J.; Coverdale, L. Proc. Natl. Acad. Sci. U.S.A. 91, 5296-5300, 1994 A; Title: Mouse stem cell antigen Sca-2 is a member of the Ly-6 family of cell surface pr A; Reference number: 148910; MUID:94261572; PMID:8202484

A;Status: preliminary; translated from GB/EMBL/DDBJ A; Accession: 148910

A; Residues: 1-136 <RE2> A; Molecule type: mRNA

A;Cross=references: EMBL:U04268; NID:g434659; PIDN:AAA19121.1; PID:g434660 C;Comment: This belongs to the Ly-6 family, a group of small cysteine-rich cell surface C;Superfamily: Ly-6 antigen; Ly-6 homology

Gaps 60; Indels 10; Query Match 22.3%; Score 144; DB 2; Length 136; Best Local Similarity 30.8%; Pred. No. 8.7e-07; Matches 40; Conservative 20; Mismatches 60; Indels 26 1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRA----V ò 셤

57 GLLTVISKGCSLNCVDDSQDYYVGKKNIT--CCDTDLCNXS----GAHALQPAAAILALL 110 67 NLGYTLNKGCSPICPSENVNLNLGVASVNSYCCQSSFCNFSAAGLGLRASIPLLGLGLLL 126 g ò

111 PALGLLLWGP 120 SLLALLQLSP 136 ò 요

phosphatidylinositol-anchored B-cell antigen ThB precursor - mouse N;Alternate names: thymocyte B-cell antigen ThB C;Species: Was musculus (house mouse) C;Bacie: 18-Jun-1993 #sequence_revision 16-Aug-1996 #text_change 28-Jan-2000 C;Accession: A46528

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A;Molecule type: mRNA
A;Residues: 25-54, A',56-62, M',64-67,'Q',69-71,'DHI',75-77,'V',79-80,'T',82-85,'T',87,'
A;Cross-references: GB:M30692, NID:g205245; PIDN:AAA1545.1; PID:g205246
A;Experimental source: clone RK6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: AMS>
A;Residues: 1-103 aMAS>
A;Cross-references: GB:X99977; NID:g1536901; PIDN:CAA68237.1; PID:e265523; PID:g1536902
A;Experimental source: placenta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Adermann, K.; Wattler, F.; Wattler, S.; Heine, G.; Meyer, M.; Forssmann, W.G.; Nehls, submitted to the Protein Sequence Database, July 1998
A;Description: Secreted protein, related to Ly-6, uPAR, soluble CD59, and snake and frog A;Reference number: A58842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 LLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRA-----VGLLTVI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARS component B 81/S protein precursor - human N;Alternate names: secreted Ly-6/UPAR related protein 1; SLURP-1 C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 29-Oct-1999 R;Magtrangeli, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ly6 homolog RK10 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 31-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Introns: 20/1; 60/1

C,Keywords: 91ycoprotein

F;1-18/Domain: signal sequence #status predicted <SIG>

F;19-22/Domain: propeptide #status predicted <PRO>

F;23-103/Product: ARS component B 81/S protein #status experimental <MAT>

F;25-50,28:37,49-99/Disulfide bonds: #status experimental <ART>

F;43-77,73-93/Disulfide bonds: (or 43-73, 77-93) #status experimental

F;43-77,73-93/Disulfide bonds: (or 43-73, 77-93) #status experimental
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A;Realdudes: 1-15 <FKI>-
A;Cross-references: GB:M30689; NID:g205247; PIDN:AAA41546.1; PID:g205248
A;Experimental gource: clone RK10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRSCSSSCVATDPDSIGAAHLIFCCFRDLCN 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, August 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 SKGCSLNCVDDSQDYYVGKKNITCCDTDLCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Description: ARS gene, component B. A; Reference number: A59031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 29.7% Matches 27; Conservative
                    106 ILALLPALGLLL 117
                                                                                                  119 SLSLLTVMALCL 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: A58842
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R;Gumley, T.P.; McKenzie, I.F.; Kozak, C.A.; Sandrin, M.S.
J. Immunol. 149, 2615-2618, 1992
A;Title: Isolation and characterization of cDNA clones for the mouse thymocyte B cell and A;Reference number: A46528; MUID:93017863; PMID:1401899
A;Accession: A46528
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-127 <GUM>A;COSSION: A6658
A;Residues: 1-127 <GUM>A;COSSION: A6658
A;Residues: 1-127 <GUM>A;COSSION: A6666; NID:9288264; PIDN:CAA45317.1; PID:9288265
A;Residues: 1-127 <GUM
A;COSSION: A6666; NID:9288264; PIDN:CAA45317.1; PID:9288265
A;COSSION: A6666; NID:9288264; PIDN:CAA45317.1; PID:9288265
A;COSSION: A6618
A;Note: sequence extracted from NCBI backbone (NCBIP:11614)
C;Generics
A;Gene: A6618
A;Note: sequence extracted from NCBI backbone (NCBIP:11614)
C;Generics
A;Gene: A6618
A;Map position: 15
C;Superfamily: Ly-6 antigen; Ly-6 homology
C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkag
F;1-20/Domain: signal sequence #status predicted <SIGS-F;21-100/Domain: Ly-6 homology <C;Keywords: blocked carboxyl end; glycoprotein; phosphatidylinositol linkag
F;21-93/Product: phosphatidylinositol-anchored B-cell antigen ThB #status predicted <ATP-F;93/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature form)
F;93/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature form)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 GNLVRKECANSCTSDYSQQGHVSSGSEVTQCCQTDLCNERLVSAAPGHALLSSVTLGLAT 115
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Cispecies: Musculus (house mouse)
Cispecies: Is a cispecies and musculus (house The gene.
Airtle: Sequence and structure of the mouse The gene.
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.larity 31.8%; Pred. No. 4.3e-05;
Conservative 19; Mismatches 51;
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A,Introns: 21/1; 54/1
C,Superfamily: Ly-6 antigen; Ly-6.homology
F;24-103/Domain: Ly-6 homology <LY6>
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Best Local Similarity 31.87
Best A2; Conservative
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Best Local S
Matches 42
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receptor; serine/threonine-specific p

31; Gaps

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y,Title: Multiple genes for Xenopus activin receptor expressed during early embryogenesi
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A;Cross-references: EMBL:Z81075; PIDN:CAB03048.1; GSPDB:GN00019; CESP:F35C12.3
A;Experimental source: clone F35C12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLLTVISKGCSL---NCVDDSQDYYVGKKN----ITCCDTDLCNXSGAH-----AL 100
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                                                                                                                                                                                                                                                                                                                                                                                             F;186-483/Domain: protein kinase homology <KIN>
F;18-202/Region: protein kinase ATP-binding motif
F;18,66/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;215/Active site: Lys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 14.9%; Score 96.5; DB 1; Length 510; Best Local Similarity 26.4%; Pred. No. 0.099; Matches 37; Conservative 22; Mismatches 50; Indels 3
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A;Introns: 53/3; 83/3; 151/3; 167/2; 198/3; 246/3; 281/2

    Caenorhabditis elegans

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                                                                                                                A; Status: not compared with conceptual translation
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||SASVLNILIYSLLPIVGL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F35C12.3 - Ca
C,Species: Caenorhabditis elegans
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Best Local Similarity 30.9%;
Matches 21; Conservative
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A;Accession: A42635
A;Accession: A42635
A;Accession: A22635
A;Accession: A22635
A;Molecule type: mRNA

A;Molecule type: mRNA

A;Molecule type: mRNA
C;Superfamily: Ly-6 antigen; Ly-6 homology C;Superfamily: Ly-6 antigen; Ly-6 homology C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkag F;1-26/Domain: signal sequence #status predicted <SIG>F;1-26/Domain: signal sequence #status predicted as amidated carboxyl end (Asn) (in mature form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD59 protein - baboon
C.Specias: Paplo sp. (baboon)
C.Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C.Accession: 136914
K.Fodor, W.L.; Rollins, S.A.; Bianco-Caron, S.; Burton, W.V.; Guilmette; E.R.; Rother,
Immunogenetics 41, 51, 1995
A;Title: Primate terminal complement inhibitor homologues of human CD59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 WTARIRAVGLLTVISKGCSLNCVD----DSQDYYVGKKNITCCDTDLCN----XSGAHALQ 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGL-- 58
                                                                                                                                                                                                                                                                                                             7 MKSCVLILLIALLCAERAQGLNCYNCTMIPFGNTCSSTATCPYPDGVC-TIQVAEVVVSS 65
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NiContains: protein kinase STK8 (BC 27.1.-)
CiSpecies: Xenopus laevis (African clawed frog)
CiSpecies: Nameries: S21233
R;Mathews, L.S.; Vale, W.W.; Kintner, C.R.
                                                                                                                                                                                                   Gaps
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A;Residues: 1-126 <RES>
A;Crose-referencese: GB:L22862; NID:g514327; PIDN:AAA74127.1; PID:g514328
C;Superfamily: Ly-6 antigen; Ly-6 homology
F;26-100/Domain: Ly-6 homology <LY6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Primate terminal complement inhibitor homologues of human CD59 A;Reference number: 136894; WUID:95104908; PMID:7528724
                                                                                                                                                                                                   9
                                                                                                                                              Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.9%; Score 96.5; DB 2; Length 126; 25.0%; Pred. No. 0.029; ive 16; Mismatches 42; Indels 4
                                                                                                                                        Query Match 15.6%; Score 100.5; DB 2; Length 1
Best Local Similarity 30.8%; Pred. No. 0.013;
Matches 32; Conservative 10; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      66 VRLKVKSNLCLPGCPKSPQTPEVLGTVVHVNTDCCNTDLCNAAG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42; Indels
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A;Note: sequence extracted from NCBI backbone (NCBIP:93126)
R;Nishimatsu, S.; Oda, S.; Murakami, K.; Ueno, N.
                                                                                                                                                                                                                                                                                                                                                                         --LTVISKGCSLNCVDDSQD----YYVGKKNITCCDTDLCNXSG
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Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 PAAAILALLPAL 113
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93

Gaps

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Length 368;

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receptor gene

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Length 222;

58

mouse

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receptor, hypothetical soluble form precursor
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    urokinase-type plasminogen activator receptor, hypothetical soluble form pro
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 23-Jul-1999
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Suh, T.T.; Nerlov, C.; Dano, K.; Degen, J.L.
Biol. Chem. 269, 25992-25998, 1999,
Title: The murine urokinase-type plasminogen activator receptor gene.
Reference number: A55356; MUID:95014420; PMID:7929309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cokinase-type plasminogen activator receptor membrane form precursor Alternate names: urokinase-type plasminogen activator receptor 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:U12235
A;Note: authors translated the codon TTG for residue 219 as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEVVIRGCAHSEKTINRIMSYRMGSMIISLTETVCATNLCN 100
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                                                                                                                                      C,Accession: B55356
R,Suh, T.T.; Nerlov, C.; Dano, K.; Degen, J.L.
J. Biol. Chem. 269, 25992-25998, 1994
A,Title: The murine urckinase-type plasminogen activator
A,Reference number: A55386; MUID:95014420; PMID:7929309
A,Accession: B55356
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14.7%; Score 95; DB 2;
Best Local Similarity 31.0%; Pred. No. 0.066;
Matches 31; Conservative 16; Mismatches 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: Ly-6 homology
C;Keywords: alternative splicing; duplication
F;24-108/Domain: Ly-6 homology <LY6>
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Best Local Similarity
Matches 31; Conserva
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Molecule type: DNA
Residues: 1-327 <SUH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-222 <SUH>
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                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
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A,Title: Two alternatively spliced mouse urokinase receptor mRNAs with different histold A,Reference number: A41643; MUID:92098587; PMID:1661735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C,Superfamily: Ly-6 antigen; Ly-6 homology
C,Keywords: blocked carboxyl end; cell adhesion; glycoprotein; lipoprotein; phosphatidyl
C;Keywords: blocked carboxyl end; cell adhesion; glycoprotein; lipoprotein; phosphatidyl
F;1-100/Domain: Ly-6 homology ~LY6->
F;21-30/Domain: Ly-6 homology ~LY6->
F;21-30/Product: E48 antigen #status predicted ~NAT->
F;21-35/Product: E48 antigen #status predicted ~NAT->
F;33-45,26-32,38-63,67-86,87-92/Disulfide bonds: #status predicted
F;93/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Asn) (in mature form)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-128 <BRA>
A;Cross-references: GB:X82693; NID:g887453; PIDN:CAA58014.1; PID:g887454
A;Note: parts of this sequence, including the amino end of the mature protein, were conf
C;Species: Homo sapiens (man)
C;Date: 08-Dec-1995 #sequence_revision 16-Aug-1996 #text_change 28-Jan-2000
C;Date: 08-Dec-1995 #sequence_revision 16-Aug-1996 #text_change 28-Jan-2000
C;Datession: A57321
R;Brakenhoff, R.H.; Gerretsen, M.; Knippels, E.M.C.; van Dijk, M.; van Essen, H.; Olde J. Cell Biol. 129, 1677-1689, 1995
A;Title: The human B48 antigen, highly homologous to the murine Ly-6 antigen ThB, is a A;Reference number: A57321 MUID:95310346; PMID:7790363
A;Reference number: A57321
A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  urokinase-type plasminogen activator receptor 2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Aug-1992 #sequefice_revision 28-Aug-1992 #text_change 05-Nov-1999
C;Accession: B41643
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A,Residues: 1-222 <KRI>
A,Cross-references: G82701; NID:g53277; PIDN:CAA44575.1; PID:g53278
C,Superfamily: Ly-6 homology
F;24-108/Domain: Ly-6 homology <LY6>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.7%; Score 95; DB 1; Length 128; 25.2%; Pred. No. 0.041; tive 15; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 8q24-qter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAL 117
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                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: B41643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59
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Matches 3
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Matches 3
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;Cross-references: GB:U12235; NID:g555809; PIDN:AAB60484.1; PID:g555810
;Kristensen, P.; Eriksen, J.; Blasi, F.; Dano, K.
. Cell Biol. 115, 1763-1771, 1991
;Title: Two alternatively spliced mouse urokinase receptor mRNAs with different histolo
;Reference number: A41643; MUID:92098587; PMID:1661735
                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns: 20/1; 57/1; 105/1; 157/1; 202/1; 251/1
C; Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology
C; Keywords: alternative splicing; duplication; glycoprotein; phosphatidylinositol linkag:
F;24-108/Domain: Ly-6 homology <LY68>
F;117-205/Domain: Ly-6 homology <LY68>
F;213-301/Domain: Ly-6 homology <LY6C>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;32,75,183,193,221,254,282/Binding site: carbohydrate (Asn) (covalent) #status predicter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 RRILLILLLATTCVPASOGLOCMOCE -- SNOSCL-VEECALGODLCRITVLREWODDRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                      A;Residues: 1-327 <KRI>
A;Cross-references: GB:X62700; NID:g441462; PIDN:CAA44574.1; PID:g441463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.7%; Score 95; DB 2; ilarity 31.0%; Pred. No. 0.093; Conservative 16; Mismatches 4
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RESULT 11 B55356

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C;Accession: C40829
R;Attisano, L.; Wrana, J.L.; Cheifetz, S.; Massague, J.
A;Title: Novel activin receptors: distinct genes and alternative mRNA splicing generate A;Reference number: A40829; MUID:92119722; PMID:1310075
     --NCVDDSQDYYVGKKN----ITCCDTDLCNXSGAHALQPAA--- 104
                                  55 AVGLLTVISKGCSL---NCVDDSQDYYVGKKN----ITCCDTDLCNXSGAHALQPAA--- 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 LALLMAGLALQPGTA-----CLCYSCKAQVSNEDCLQVENCTQLGEQ-----CWTARIR 54
                                                                                                                                                                                                                                                                                                   activin receptor isoform IIB3 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 23-May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 LALLWGSLCAGSGRGEAETRECIYYNANWELERTNQSGLERCE--GEQDKRLHCYASWRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:88362, NCBIP:88363)
C;Superfamily: activin receptor II; protein kinase homology
C;Keywords: ATP; receptor
F;204-501/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 528;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 14.6%; Score 94; DB 2;
Best Local Similarity 26.6%; Pred. No. 0.18;
Matches 37; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: August 18, 2003, 19:44:25 Job time : 40 Becs
                                                                                                            ----AILA--LLPALGLLL 117
                                                                                                                                                                125 PTLLTVLAYSLLPIGGLSL 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----AILA--LLPALGLLL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 PTLLTVĽÁYSĽĽPIGGĽSĽ 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-528 <ATT>
A;Experimental source: Balb/c 3T3
     55 AVGLLTVISKGCSL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary
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                                                                                                                                                                                                           C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 28-May-1999
C;Accession. 553340; S53339.
R;Rubimere, N.K.; Harrison. R.A.; van den Berg, C.W.; Morgan, B.P.
Biochem. J. 304, 595-601, 1994
A;Title: Molecular cloning of the rat analogue of human CD59: structural comparison with A;Reference number: S53339; MUID:95091697; PMID:7528012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: protein
A;Residues: 23-224, X', 26-27, X', 29-34, X', 36-37, 'X', 39-40, 'X';42-47, 'X', 49-58, 'X', 60, 'XR
C;Superfamily: Ly-6 antigen; Ly-6 homology
F;23-101/Domain: Ly-6 homology <LY6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activin receptor isoform IIB4 - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: O4-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 23-May-1997
C;Accession: B40829
R;Attisano, L.; Wrana, J.L.; Cheifetz, S.; Massague, J.
A;Attisano, L.; Wrana, J.L.; Cheifetz, S.; Massague, J.
A;Title: Novel activin receptors: distinct genes and alternative mRNA splicing generate A;Reference number: A40829; MUID:92119722; PMID:1310075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 ARIRAVGLITVISKGCSLNCVDDSQDYYVGKKNITCCDTDLCNXS------GAHALQPA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -RFSDCNAKFILSR-----LEIANVQYRCCQADLCNKSFEDKPNNGAISLLGK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 KAVLLALLMAGLALQPGTALLCYSCKAQVSN------EDCLQVENCTQLGEQCWT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 LALLWGSLCAGSGRGEAETRECIYYNANWELERTNQSGLERCE--GEQDKRLHCYASWRN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GB:U48455; NID:g1199654; PIDN:AAA88909.1; PID:g1199655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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A; Residues: 1-504 <ATT>
A; Experimental source: Balb/c 3T3
A; Note: sequence inconsistent with the nucleotide translation
A; Note: sequence extracted from NCBI backbone (NCBIN:88364, NCBIP:88365)
C; Superfamily: activin receptor II; protein kinase homology
C; Keywords: ATP; receptor
F;180-477/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.6%; Score 94.5; DB 2; Length 126; 25.8%; Pred. No. 0.045; tive 16; Mismatches 43; Indels 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.6%; Score 94; DB 2; Length 504; 26.6%; Pred. No. 0.17; tive 19; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 LALLMAGLALQPGTA-----LLCYSCKAQVSNEDCLQVENCTQLGEQ
                            | | |:::||:
LEVVTRGCAHSEKINRIMSYRMGSMIISLIETVCATNLCN 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 25.8 Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-126 <RUS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAIL 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
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29
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: August 18, 2003, 19:41:59 ; Search time 23 Seconds (without alignments)

139.807 Million cell updates/sec

139.807 Million cell upd US-09-934-586A-2

Title: US-09-934-586A-2 Perfect score: 646 Sequence: 1 MKAVLLALIMAGLALQPGTA......AAILALLPALGLLLWGPGQL 123

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 123791 segs, 26142687 residues Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database : Pending Patents AA New:*

1: /cgn2_6/ptodata/1/paa/USO6_NEW_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/USO6_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/USO8_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/USO9_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/USO9_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/USO9_NEW_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/USO9_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		* Query			00.475.00	
Š.	Score	Match	Length	BB	ΙD	Description
٦	441	68.3	88	9	US-10-631-402-2576	Sequence 2576, Ap
~	441	68	88	9	US-10-631-441-2576	Sequence 2576, Ap
m	158.5	~	131	Н	PCT-US02-29560A-346	346,
4	158.5	24	131	۲	US-60-485-450-1070	107
ഗ	158.5	~	131	1	US-60-490-890-1489	1489,
9	128.5		116	9	US-10-286-897-2973	297
7	128.5	Н	116	9	US-10-258-898A-2973	297
60	128.5	Н	128	9	US-10-286-897-6545	ø
Ø	128.5	-	128	9	US-10-258-898A-6545	654
10	117.5	-	141	Н	PCT-US03-18400-14	14,
1	117.5	18.2	141	Н	PCT-US02-29560A-322	32
12	117.5	18.2	141	7	US-60-490-890-1833	1833
13	104.5	-	162	-1	PCT-US03-21703-97	97,
14	102.5	H	227	Н	PCT-US03-18400-17	17,
15	101	-	125	9	US-10-621-401-169	М
16	97.5	٦	146	Н	PCT-US03-21703-100	100
17	96.5	-	86	7	US-60-485-450-1071	107
18	95.5	Н	94	9	US-10-273-573-7711	
13	92.5	-	128	9	US-10-408-765A-1118	Sequence 1118, Ap
20	91.5	-	191	9	US-10-273-573-7712	
21	90	Н	155	Н	PCT-US03-21703-86	86,
22	90		176	-	PCT-US03-21703-83	83,
23	90	13.9	248	9	US-10-273-573-7513	7513
24	88.5	13.7	174	~	PCT-US03-21703-93	93,
25	88.5	13.7	195	-	PCT-US03-21703-90	Sequence 90, Appl
56	88.5	13.7	195	Н	PCT-US03-21703-104	104

Sequence 3096, Ap Sequence 3096, Ap Sequence 6668, Ap Sequence 87, Appl Sequence 94, Appl Sequence 102, App Sequence 102, App Sequence 102, App Sequence 1653, App Sequence 3820, App Sequence 3820, App Sequence 6863, App Sequence 6863, App Sequence 1853, App Sequence 1853, App Sequence 1853, App Sequence 6863, App Se	Sequence 3291, Ap
US-10-286-897-3096 US-10-258-898A-3096 US-10-258-898A-3096 US-10-258-898A-6668 PCT-US03-21703-87 PCT-US03-21703-94 PCT-US03-21703-94 PCT-US03-21703-102 US-60-485-450-1652 US-60-485-450-1653 US-60-485-450-1653 US-60-485-450-1653 US-10-293-244-3821 US-10-293-244-3821 US-10-293-244-3821 US-10-293-244-3821 US-10-293-244-3821 US-10-293-244-3821 US-10-293-244-3821 US-10-293-244-3821 US-10-293-244-3821 US-10-293-244-3821 US-10-293-244-3821 US-10-293-244-3821 US-10-293-244-3821 US-10-293-244-3823 US-10-293-244-1853	US-10-258-898A-3291
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ALIGNMENTS

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US-10-63-402-5576

Sequence 2576, Application US/10631402

Sequence 2576, Application US/10631402

Sequence 2576, Application US/10631402

APPLICANT: Dunds Mile Edwards, Jean Baptiste
APPLICANT: Dunds Mile Edwards, Jean Baptiste
APPLICANT: Dunds Mile Edwards, Jean Baptiste
APPLICANT: Dunds Mile Edwards, Jean Baptiste
APPLICANT: Dunds Mile Expressed Sequence Tags and Encoded Human Proteins
FURBENT FILING DATE: 2000-07-30

PRIOR PLILOX DATE: 2000-04-109/547,599C

PRIOR PLILOX DATE: 1997-08-01
PRIOR PLILOX DATE: 1997-08-01
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PRIOR PLILOX DATE: 1
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NAME/KEY: UNSURE
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APPLICANT: Duclert, Aymeric
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APPLICANT: Duclert, Aymeric
APPLICANT: Duclert, Aymeric
APPLICANT: Duclert, Aymeric
APPLICANT: Lacroxx, Bruno
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
FILE REFERENCE: GEN-T119C1
CURRENT FILING DATE: 2003-07-30
PRIOR PLICATION NUMBER: US/09/547,599C
PRIOR APPLICATION NUMBER: US 08/905,23
PRIOR PILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,051
PRIOR PILING DATE: 1997-08-01
PRIOR PILING DATE: 1997-08-01
PRIOR PELING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,144
PRIOR PILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,134
PRIOR PILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,134
PRIOR PILING DATE: 1997-08-01
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Pred. No. 1.2e-42;
0; Mismatches 4.
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LOCATION: 58
OTHER INFORMATION: Xaa = Asp,His
FEATURE:
                              NAME/KEY: UNSURE
LOCATION: 16
OTHER INFORMATION: Xaa = Gly,Ser
                                                                                                                               NAME/KEY: UNSURE
LOCATION: 12
; OTHER INFORMATION: Xaa = Lyg, Arg
US-10-631-402-2576
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 95.5%;
Matches 84; Conservative
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LOCATION: -15..-1
OTHER INFORMATION:
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OTHER INFORMATION:
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60 TV----ISKGCSLNC-VDDSQDYYVGKKNITCCDTDLCNXSGAH-----ALQPAAAIL 107
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APPLICANT: Afar, Daniel
APPLICANT: Gish, Kurt C.
APPLICANT: Milson, Keith E.
APPLICANT: Milson, Keith E.
APPLICANT: Milson, Keith E.
APPLICANT: Bos Biotechnology, Inc.
APPLICANT: Bos Biotechnology, Inc.
APPLICANT: Bos Biotechnology, Careening for Modulators of Cancer; TITLE OF INVENTION: Methods of Diagnosis of Cancer; PTLE REFERENCE: 018501-002710PC; CURRENT PFLING DATE: 2002-09-17
PRIOR PPLING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: DCT/US02/29560A; CURRENT FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: US 60/323,469
RIOR APPLICATION NUMBER: US 60/323,469
SPIWARE: FastERQ for Windows Version 3.0
SOFTWARE: FastERQ for Windows Version 3.0
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                                                                                                                                                                                                              Length 88;
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; GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: CHANG, Sheng-Yung
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53;
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Best Local Similarity 95.5%; Pred. No. 1.2e-42;
Matches 84; Conservative 0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18; Mismatches
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CTHER INFORMATION: Xaa = Gly, Ser | FEATURE:
NAME/KEY: UNSURE
LOCATION: 12
OTHER INFORMATION: Xaa = Ly8, Arg
US-10-631-441-2576
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Best Local Similarity 35.39
Matches 47; Conservative
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TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO1470
CURRENT APPLICATION NUMBER: US/60/485,450
CURRENT FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 47859
SOFTWARE: FactSEQ for Windows Version 4.0
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APPLICANT: Rupnow, Brent A.
APPLICANT: Webster, Kevin R.
APPLICANT: Jackson, Donald
APPLICANT: Jackson, Donald
TITLE OF INVENTION: BIOMARKERS OF CYCLIN-DEPENDENT KINASE MODULATION
FILE REFERENCE: D0310 PSP
CURRENT FILING DATE: 2003-07-29
NUMBER OF SEQ ID NOS: 2779
SOFTWARE: Patentin version 3.2
TENNOM: TENNOM: APPLICANT OF SEQ ID NOS: 2779
SEQ ID NO 1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRA-VGLL
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                                                                                                                                                                                                                                                                                                                 DB 7; Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 131;
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                                                                                                                                                                                                                                                                                                               24.5%; Score 158.5; DB 7 35.3%; Pred. No. 8.5e-11; tive 18; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2973, Application US/10286897 GENERAL INFORMATION:
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121 SLLPA--LLRFGP 131
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Best Local Similarity 35.34
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 35.3*
Matches 47; Conservative
                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
US-60-485-450-1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
US-60-490-890-1489
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FRICK RAPLICATION NUMBER 18/50/48,725

FRICK PADELATION NUMBER 18/50/48,725

FRICK PADELATION NUMBER 18/50/48,725

FRICK PADELATION NUMBER 18/50/48,725

FRICK PADELATION NUMBER 18/50/58,430

FRICK PADELATION NUMBER 18/50/58,430

FRICK PADELATION NUMBER 18/50/58,430

FRICK PADELATION NUMBER 18/50/58,340

FRICK PADELATION NUMBER 18/50/58,340

FRICK PADELATION NUMBER 18/50/58,340

FRICK PADELATION NUMBER 18/50/58,340

FRICK PADELATION NUMBER 18/50/59,3036

FRICK PADELATION NUMBER 18/50/59/59,3036

FRICK PADELATION NUMBER 18/50/50/312

FRICK PADELATION NUMBER 18/50/50/312

FRICK PADELATION NUMBER 18/50/50/312

FRICK PADELATION NUMBER 18/50/50/313

FRICK PADELATION NUMBER 18/50/50/
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US-10-258-898A-6545
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                                                                                                                                                                                                                                                                                                                                                                                                                                  59 KVSKSCVPRCFETVYDGYSKHASTTSCCOYDLCNGTGL----ATPATLALAPILLATLWG 114
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JAPLICANT: Hysesq Inc.

TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
FILE REFERENCE: 784FLPCT
CURRENT PELLING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: US/09/488,725
PRIOR APPLICATION NUMBER: US/09/552,317
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR PELLOATION NUMBER: US/09/653,450
PRIOR APPLICATION NUMBER: US/09/65,191
PRIOR PELLOATION NUMBER: US/09/65,191
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-09-14
PRIOR PELLOATION NUMBER: US/09/693,036
PRIOR FILING DATE: 2000-09-14
PRIOR PELLOATION NUMBER: US/09/693,036
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7143
SOFTWARE DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER DE FLEGGENER
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GENERAL INFORMATION:
APPLICANT: Hyseq Inc
TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
FILE REFERENCE: 784FLECT
CURRENT APPLICATION NUMBER: US/10/258,898A
CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: US/99/488,725
PRIOR APPLICATION NUMBER: US/99/488,725
PRIOR APPLICATION NUMBER: US/99/488,725
PRIOR APPLICATION NUMBER: US/99/488,725
                                                                                                                                            13; Mismatches
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                                                                                                      Best Local Similarity 30.0
Matches 36; Conservative
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; ORGANISM: Homo sapiens
US-10-286-897-6545
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Best Local Similarity
Matches 36; Conserval
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US-10-258-898A-2973
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US-10-286-897-6545
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61 VISKGCSLNCVDDSQDYYVGKKNIT-CCDTDLCNXSGAHALQPAAAILALLPALGLLLWG 119
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TITLE OF INVENTION: Cancer-Linked Gene as Target for Chemotherapy
FILE REFERENCE: 689290-158
CURRENT APPLICATION UNMER: PCT/US03/18400
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: US/60/388,157
PRIOR FILING DATE: 2002-06-12
NUMBER OF SEQ ID NOS: 18
SEQ ID NOS: 18
LENGTHARE: Patentin version 3.0
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 141;
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18.2%; Score 117.5; DB 1
Best Local Similarity 32.8%; Pred. No. 3.6e-06;
Matches 43; Conservative 13; Mismatches 5¢
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19.9%; Score 128.5; DB 6
Best Local Similarity 30.0%; Pred. No. 1.9e-07
Matches 36; Conservative 13; Mismatches 6
PRIOR APPLICATION NUMBER: USO9/620,312
PRIOR APPLICATION NUMBER: USO9/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-08-31
PRIOR PILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: USO9/662,191
PRIOR APPLICATION NUMBER: USO9/662,191
PRIOR FILING DATE: 2000-09-14
PRIOR FILING DATE: 2000-10-19
PRIOR FILING DATE: 2000-11-29
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7143
SOFTWARE: DE FL_Genes_b Versions 1.0
SEQ ID NO 6545
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PCT-US02-29560A-322
; Sequence 322, Application PC/TUS0229560A
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PCT-US03-18400-14
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ORGANISM: Homo sapiens
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38; Conservative
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APPLICANT: Wang, Jianrui
APPLICANT: Zhou, Ping
APPLICANT: Wehrman, Tom
APPLICANT: Wang, Zhiwei
APPLICANT: Tang, Y. Tom
       105 AILALLPALGL 115
                                                  126 RTTIĽFLKĽAĽ 136
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Best Local Similarity
Matches 38; Conserv
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PCT-US03-18400-17
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                                      APPLICANT: Gish, Kurt C.
APPLICANT: Hevezi, Peter A.
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Mack, David H.
APPLICANT: Solonik, Albert
APPLICANT: Solonik, Albert
APPLICANT: Ess Biotechnology, Inc.
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-002710PC
CURRENT FILING DATE: 2002-09-17
CURRENT FILING DATE: 2002-09-17
PRIOR PLICATION NUMBER: US 60/323,469
PRIOR FILING DATE: 2001-09-17
NUMBER OF SEQ ID NOS: 412
SOCTUMENT FALLING VAINGOME VERSION 3.0
SEQ ID NOS: 412
FUNDER OF SEQ ID NOS: 412
FUNDER OF SEQ ID NOS: 412
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FUNDER OF SEQ ID NOS: 412
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APPLICANT: Webster, Kevin R.
APPLICANT: Webster, Kevin R.
APPLICANT: Webster, Kevin R.
APPLICANT: Jackson, Donald
APPLICANT: Jackson, Donald
APPLICANT: Wong, Tai W.
TITLE OF INVENTION: BIOMARKERS OF CYCLIN-DEPENDENT KINASE MODULATION
FILE REFERENCE: D0310 PSP
CURRENT APPLICATION NUMBER: US/60/490, 890
CURRENT FILING DATE: 2003-07-29
NUMBER OF SEQ ID NOS: 2779
SOFTWARE: Patentin version 3.2
LENGTH: 141
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32.8%; Pred. No. 3.6e-06;
iive 13; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1813, Application US/60490890
GENERAL INFORMATION:
APPLICANT: Li, Martha
Afar, Daniel
Aziz, Natasha
Gish, Kurt C.
Hevezi, Peter A.
Mack, David H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43; Conservative
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US-60-490-890-1833
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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Matches 43; Conserva
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Best Local Similarity
Matches 43; Conserv
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56 VGLLTVISKGCSLNCVDDSQDY-----YVGKKNITCCDTDLCNXSGAHALQPAAAILA 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2002-10-11
PRIOR APPLICATION WUMBER: PCT/US02/39555
PRIOR FILING DATE: 2002-12-10
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 110
SOFWBARE: PatentIn version 3.1
SEQ ID NO 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application PC/TUS0318400
GENERAL INFORMATION:
BPPLICANT: Avalon Pharmaceuticals
TITLE OF INVENTION: Cancer-Linked Gene as Target for Chemotherapy
FILE REFERENCE: 689290-158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.2%; Score 104.5; DB 1; Length 162; 28.4%; Pred. No. 0.00012;
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Sequence 97, Application PC/TUS0321703 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               159 SSAACLIASAGYQSFCSPGKLNSVCISCCNTPLCNGPRPKKRGSSASALRPGLRTTILFL 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 CSLNCVDDSQDYY----VGKKN---ITCCDTDLCN-----XSGAHALQPAAAILALLP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 AGLALQPGTALLCYSCKAQVSNEDCLQVE---NCT-QLGEQCWTARI-RAVGLLTVISKG 65
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PRIOR FILING DATE: 1998-11-04
PRIOR FILING DATE: 1998-11-04
PRIOR FILING DATE: 1998-11-04
PRIOR PRILING DATE: 1997-11-07
PRIOR PPLICATION NUMBER: US 60/064,911
PRIOR PELING DATE: 1997-11-07
PRIOR PELING DATE: 1997-11-07
PRIOR PELING DATE: 1997-11-07
PRIOR PELING DATE: 1997-11-07
PRIOR PILING DATE: 1997-11-07
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                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 15.9%; Score 102.5; DB 1; Length 227; Best Local Similarity 31.5%; Pred. No. 0.0003; Matches 39; Conservative 13; Mismatches 49; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE TO INVENTION: 125 Human Secreted Proteins FILE REFERENCE: PZ020P2C1.
CURRENT APPLICATION NUMBER: US/10/621,401
CURRENT PILING DATE: 2003-07-18
FRIOR PILING DATE: 2003-07-18
FRIOR PELICATION NUMBER: US 09/974,879
FRIOR FILING DATE: 2001-01-01
FRIOR PELICATION NUMBER: US 09/818,683
FRIOR PELICATION NUMBER: US 09/818,683
FRIOR PELING DATE: 2001-03-28
FRIOR APPLICATION NUMBER: US 09/818,736
FRIOR PELING DATE: 1999-05-05
FRIOR FILING DATE: 1999-05-05
FRIOR FILING DATE: 1999-10-04
CURRENT APPLICATION NUMBER: PCT/US03/18400
                        CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: US/60/388,157
PRIOR FILING DATE: 2002-06-12
NUMBER OF SEQ ID NOS: 18
SEG ID NO 17
LENGTH: 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 169, Application US/10621401
; GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-10-621-401-169
                                                                                                                                                                                                                                                                TYPE: PRT
CORGANISM: Homo sapiens
PCT-US03-18400-17
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US-10-621-401-169
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1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENC-TQLGEQCWTARIRAVGLL 59

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Db 1 WKALML-LTLSVLLCWVSADIRCHSC-YKVPVLGCVDRQSCRLEPGQQCLTTH-AYLGKM 57

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Qy 110 LPALGLLLW 118

Db 114 TSLAGLGLW 122

Search completed: August 18, 2003, 19:51:55

Job time: 23 secs
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Sequence 2, Application US/09564129A
Paceure No. US2001005751A1
GENERAL INFORMATION: Wite, Owen N.
APPLICANT: Raiter, Robert E.
APPLICANT: Raiter, Robert E.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFREENCE: 304353.540S14
CURRENT FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 08/814,279
PRIOR APPLICATION NUMBER: 66/071,141
PRIOR FILING DATE: 1998-01-22
PRIOR FILING DATE: 1998-01-22
PRIOR PRILING DATE: 1998-01-23
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PRIOR PRILING DATE: 1998-02-13
PRIOR PRILING DATE: 1998-02-17
PRIOR PRILING DATE: 1998-02-17
PRIOR APPLICATION NUMBER: 60/120,536
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PRIOR PRILING DATE: 1999-03-10
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646
1 MKAVLLALJMAGLALQPGTA.....AAILALLPALGLLLWGPGQL 123
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Sequence 6,
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3: /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-884-811-2
US-09-934-773-5
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US-09-564-329A-6
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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US-09-934-773-4
US-09-934-773-4
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US-09-934-586A-5
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Query Match 99.8%; Score 645; DB 10; Length 123; Best Local Similarity 99.2%; Pred. No. 1.1e-62; Matches 122; Conservative 0; Mismatches 1; Indels (
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FEATURE:
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NAME/KEY: SITE
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Pred. No. 1.1e-62;
0; Mismatches 1; Indels
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Pred. No. 1.1e-62;
0; Mismatches 1;
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; ORGANISM: HUMAN PSCA (hPSCA)
US-09-564-329A-6
ORGANISM: HUMAN PSCA (hPSCA)
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Best Local Similarity 99.2
Matches 122; Conservative
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Best Local Similarity 99.2
Matches 122; Conservative
                                                      ; NAME/KEY: SITE
; LOCATION: (50)...(64)
; LOCATION: (71)...(82)
; LOCATION: (71)...(82)
; NAME/KEY: SITE
; LOCATION: (67)...(81)
US-09-564-329A-2
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61 VISKGCSLNCVDDSQDYYVGKKNITCCDTDLCNXSGAHALQPAAAILALLPALGLLLWGP 120
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Patent No. US2020102666A1
GRERAL INCRMATION:
APPLICANT: Reiter: Robert E.
APPLICANT: Witte, Owen N.
APPLICANT: Witte, Owen N.
APPLICANT: Witte, Owen N.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF FILE REPERFENCE: 30435.540814
CURRENT APPLICATION NUMBER: US/09/855,153
CURRENT FILING DATE: 2000-05-03
PRIOR FILING DATE: 2000-05-03
PRIOR FILING DATE: 1999-07-20
PRIOR PILING DATE: 1999-01-12
PRIOR PILING DATE: 1999-01-12
PRIOR PILING DATE: 1999-01-12
PRIOR PILING DATE: 1999-02-17
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PRIOR PILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
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61 VISKGCSLNCVDDSQDYYVGKKNITCCDTDLCNXSGAHALQPAAAILALLPALGLLLWGP 120
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Patent No. US20020119157A1

GENERAL INFORMATION:
APPLICANT Reiter. Robert E.
APPLICANT Witte, Owen N.
APPLICANT Saffran, Douglas C.
ITTLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
ITTLE OF INVENTION PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
ITTLE PREERENCE: 30435-54US14

CURRENT APPLICATION NUMBER: US/09/854,811

CURRENT FILING DATE: 2001-05-14

PRIOR PELICATION NUMBER: 09/359,326

PRIOR APPLICATION NUMBER: 09/359,326

PRIOR APPLICATION NUMBER: 09/359,326

PRIOR SEQ ID NOS: 27

SOFTWARE PATENT VET: 2.00

SEQ ID NOS: 27

SOFTWARE PATENT NOS: 27
                      GENERAL INFORMATION:
APPLICANT: Relter, Robert E.
APPLICANT: Witter, Owen N.
APPLICANT: Witter, Owen N.
APPLICANT: Gaffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF FILE REFERENCE: 30435-540S14.
FILE REFERENCE: 2001-05-14
FILE REPERENCE: 2001-05-14
PRIOR PILING DATE: 2001-05-03
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
SOFTWARE: PATENTING OF SEQ ID NOS: 27
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Pred. No. 1.1e-62;
0; Mismatches 1; Indels
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Best Local Similarity 99.2%; Pred. No. 1.1e-62;
Matches 122; Conservative 0; Mismatches 1;
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Best Local Similarity 99.2%;
Matches 122; Conservative 0
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US-09-854-811-6
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Patent No. US20020119157A1
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NAME/KEY: SITE
LOCATION: (71)..(82)
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61 VISKGCSLNCVDDSQDYYVGKKNITCCDTDLCNXSGAHALQPAAAILALLPALGLLLWGP 120
                                   61 VISKGCSLNCVDDSQDYYVGKKNITCCDTDLCNASGAHALQPAAAILALLPALGLLLWGP 120
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GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Witch, Owen N.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF FILE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF CURRENT FILING DATE: 2001-05-14

PRIOR PLILOK DATE: 2001-05-03
PRIOR APPLICATION NUMBER: 09/564,329
PRIOR PLILOK DATE: 1999-07-20
PRIOR PLILING DATE: 1999-07-20
PRIOR PLILING DATE: 1999-07-20
PRIOR PLILING DATE: 1999-01-12
PRIOR PLILING DATE: 1999-01-13
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PRIOR PLILING DATE: 1999-02-17
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; Sequence 6, Application US/09855153
; Patent No. US20020102666A1
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ORGANISM: HUMAN PSCA (hPSCA)
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APPLICANT: Mitte, Owen N.
APPLICANT: Mitte, Owen N.
APPLICANT: Mitte, Owen N.
APPLICANT: Seiffran, Douglas C.
TITLE OF INVENTION: SCCA: PROCRATE STEM CELL ANTIGEN AND USES THEREOF FILE OF INVENTION: SCCA: PROCRATE STEM CELL ANTIGEN AND USES THEREOF CURRENT PELLING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: 09/564,329
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 09/359,326
PRIOR APPLICATION NUMBER: 06/071,141
PRIOR APPLICATION NUMBER: 60/071,141
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR PELLING DATE: 1999-03-16
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Pred. No. 1.1e-62;
0; Mismatches 1;
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US-09-963-620-2
Sequence 2, Application US/09963620
; Patent No. US20020141941A1
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Best Local Similarity 99.2%;
Matches 122; Conservative
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ORGANISM: HUMAN PSCA (hPSCA)
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Patent No. US20020136689A1

GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REPERENCE: 30435, 544132
PRIOR APPLICATION NUMBER: US/09/934,773

CURRENT APPLICATION NUMBER: US/09/934,773

CURRENT APPLICATION NUMBER: 09/564,329
PRIOR APPLICATION NUMBER: 09/564,329
PRIOR APPLICATION NUMBER: 09/359,326

PRIOR APPLICATION NUMBER: 60/014,675

PRIOR APPLICATION NUMBER: 60/014,675

PRIOR APPLICATION NUMBER: 60/11,141

PRIOR APPLICATION NUMBER: 60/113,200

PRIOR PILING DATE: 1999-02-13

PRIOR FILING DATE: 1999-02-16

PRIOR FILING DATE: 1999-02-16

PRIOR FILING DATE: 1999-02-16

PRIOR FILING DATE: 1999-02-17

PRIOR APPLICATION NUMBER: 60/124,658

PRIOR PRILING DATE: 1999-02-17

PRIOR APPLICATION NUMBER: 09/203,939

PRIOR PRILING DATE: 1999-02-17

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ORGANISM: HUMAN PSCA (hPSCA)
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Matches 122, Conservative
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61 VISKGCSLNCVDDSQDYYVGKKNITCCDTDLCNASGAHALQPAAAILALLPALGLLLMGP 120
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Publication No. US20030113818A1
GENERAL INFORMATION:
APPLICANT: Witch, Owen N.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REPERENCE: 30435.54US14
CURRENT APPLICATION NUMBER: US/99/855,632
CURRENT FILING DATE: 2001-05-14
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Pred. No. 1.1e-62;
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                          CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/564,329
PRIOR APPLICATION NUMBER: 09/564,329
PRIOR APPLICATION NUMBER: 09/359,326
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR PLING DATE: 1998-01-12
PRIOR PLING DATE: 1998-01-12
PRIOR PLING DATE: 1998-01-13
PRIOR PLING DATE: 1998-01-13
PRIOR PLING DATE: 1998-01-13
PRIOR PILING DATE: 1998-02-13
PRIOR PILING DATE: 1998-02-13
PRIOR PILING DATE: 1998-02-17
PRIOR PLING DATE: 1999-03-16
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PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 09/359,326
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: 08/814,279
PRIOR FILING DATE: 1997-03-10
PRIOR PELING DATE: 1998-01-12
PRIOR FILING DATE: 1998-01-12
PRIOR APPLICATION NUMBER: 60/071,141
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Best Local Similarity 99.2%;
Matches 122; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORGANISM: HUMAN PSCA (hPSCA)
US-09-963-620-6
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US-09-855-632-2
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                                              APPLICANT: MITCE, Owen No.

APPLICANT: MITCE, Owen No.

TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

FILE REPERENCE: 30435.541814

CURRENT APPLICATION NUMBER: 09/964,329

PRIOR FILING DATE: 2000-05-03

PRIOR APPLICATION NUMBER: 09/359,326

PRIOR APPLICATION NUMBER: 09/359,326

PRIOR APPLICATION NUMBER: 09/359,326

PRIOR PILING DATE: 1999-07-20

PRIOR FILING DATE: 1999-07-10

PRIOR FILING DATE: 1998-01-12

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-17

PRIOR FILING DATE: 1998-02-17

PRIOR FILING DATE: 1999-03-16

PRIOR FILING DATE: 1999-02-17

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APPLICANT: Witte, Owen N.
APPLICANT: Saffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
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Pred. No. 1.1e-62;
0; Mismatches 1; Indels
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Patent No. US20020141941A1
GENERAL INFORMATION:
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Best Local Similarity 99.2%;
Matches 122; Conservative
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CANT: Reiter, Robert E. CANT: Witte, Owen N.
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US-09-963-620-6
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Wite, Owen N.
TITLE OF INVENTION: PECA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30415,541814
CURRENT APPLICATION NUMBER: US/10/224,720
CURRENT APPLICATION NUMBER: US/09/359,326
PRIOR PELING DATE: 1999-07-20
PRIOR PELING DATE: 1999-07-20
PRIOR PELING DATE: 1999-07-30
PRIOR PELING DATE: 1998-01-12
PRIOR PELING DATE: 1998-01-12
PRIOR PELING DATE: 1998-02-13
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                          PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 09/038,261
PRIOR APPLICATION NUMBER: 09/203,939
PRIOR PILING DATE: 1998-12-02
PRIOR FILING DATE: 1998-12-02
PRIOR FILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-02-17
PRIOR FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 6
LENGTH: 123
APPLICATION NUMBER: 60/124,658
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Sequence 2, Application US/10224720
Publication No. US20030147806A1
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; ORGANISM: HUMAN PSCA (hPSCA)
US-09-855-632-6
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LENGTH: 123
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APPLICANT Reiter. Robert E.
APPLICANT Witte, Owen N.
APPLICANT SAffran, Douglas C.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF TILE REFERENCE: 30435.540S14
CURRENT APPLICATION NUMBER: US/09/855,632
CURRENT PILING DATE: 2000-05-14
CURRENT PILING DATE: 2000-05-14
CURRENT FILING DATE: 2000-05-03
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1998-01-12
PRIOR FILING DATE: 1998-01-12
PRIOR FILING DATE: 1998-01-12
PRIOR FILING DATE: 1998-01-13
PRIOR FILING DATE: 1998-01-13
PRIOR FILING DATE: 1998-01-13
PRIOR APPLICATION NUMBER: 60/011,141
PRIOR FILING DATE: 1998-01-13
PRIOR APPLICATION NUMBER: 60/113,230
PRIOR APPLICATION NUMBER: 60/113,230
PRIOR APPLICATION NUMBER: 60/113,230
PRIOR APPLICATION NUMBER: 60/110,536
PRIOR FILING DATE: 1999-02-17
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   PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 60/113,230
PRIOR PILLING DATE: 1998-12-21
PRIOR APPLICATION NUMBER: 60/120,536
PRIOR FILING DATE: 1999-02-17;
PRIOR FILING DATE: 1999-03-16
PRIOR PILING DATE: 1999-03-16
PRIOR PILING DATE: 1998-03-16
PRIOR APPLICATION NUMBER: 09/038,261
PRIOR APPLICATION NUMBER: 09/23,339
PRIOR PILING DATE: 1998-02-17
PRIOR PILING DATE: 1998-12-02
PRIOR PILING DATE: 1998-02-17
PRIOR PILING DATE: 1999-02-17
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SOFTWARE: PARENTIN Ver: 2.0
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Publication No. US20030113818A1
GENERAL INFORMATION:
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ORGANISM: HUMAN PSCA (hPSCA)
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; LOCATION: (67)..(81)
US-09-855-632-2
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NAME/KEY: SITE
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APPLICANT: Witte, Owen N.
APPLICANT: Witte, Owen N.
APPLICANT: Witte, Owen N.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.540S14
CURRENT PAPLICATION NUMBER: US/10/225,784
CURRENT PAPLICATION NUMBER: US/09/564,329
PRIOR APPLICATION NUMBER: US/09/564,329
PRIOR APPLICATION NUMBER: 08/01/20
PRIOR PILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-30
PRIOR PLILING DATE: 1999-07-30
PRIOR PLILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 60/074,675
PRIOR APPLICATION NUMBER: 60/113,230
PRIOR PLILING DATE: 1998-02-17
PRIOR APPLICATION NUMBER: 60/113,230
PRIOR APPLICATION NUMBER: 60/120,536
PRIOR PLILING DATE: 1998-02-17
PRIOR PLILING DATE: 1998-02-17
PRIOR PLILING DATE: 1998-02-17
PRIOR PLILING DATE: 1998-03-16
PRIOR PLILING DATE: 1998-03-16
PRIOR APPLICATION NUMBER: 60/120,536
PRIOR PLILING DATE: 1998-03-16
PRIOR APPLICATION NUMBER: 09/038,261
PRIOR APPLICATION NUMBER: 09/038,261
PRIOR APPLICATION NUMBER: 09/038,261
PRIOR APPLICATION NUMBER: 09/038,261
PRIOR APPLICATION NUMBER: 09/038,261
PRIOR APPLICATION NUMBER: 09/038,261
PRIOR PLILING DATE: 1998-03-10
PRIOR PLILING DATE: 1998-03-10
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PRIOR PLILING DATE: 1998-03-10
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SEQ ID NOS: 27
PatentIn Ver. 2.0
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Publication No. US20030113820A1
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ORGANISM: HUMAN PSCA (hPSCA)
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Matches 122, Conservative
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LOCATION: (67)
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FILE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
TITLE OF INVENTION NUMBER: US/10/224,720
CURRENT FILING DATE: 1999-07-03-06
FRIOR PAPLICATION NUMBER: US/09/389,326
FRIOR PAPLICATION NUMBER: US/09/389,326
FRIOR PAPLICATION NUMBER: 08/814,279
FRIOR PAPLICATION NUMBER: 08/814,279
FRIOR PAPLICATION NUMBER: 06/071,141
FRIOR APPLICATION NUMBER: 60/071,141
FRIOR APPLICATION NUMBER: 60/113,230
FRIOR APPLICATION NUMBER: 60/113,230
FRIOR APPLICATION NUMBER: 60/113,230
FRIOR APPLICATION NUMBER: 60/124,658
FRIOR APPLICATION NUMBER: 60/124,658
FRIOR APPLICATION NUMBER: 09/23,339
FRIOR APPLICATION NUMBER: 09/23,339
FRIOR APPLICATION NUMBER: 09/23,339
FRIOR PELING DATE: 1999-03-16
FRIOR PELING DATE: 1999-03-16
FRIOR PELING DATE: 1999-03-16
FRIOR FILING DATE: 1999-03-16
FRIOR FILING DATE: 1999-03-16
FRIOR FILING DATE: 1999-02-17
FRIOR FILING DATE: 1999-02-17
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Pred. No. 1.1e-62;
0; Mismatches 1; Indels (
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Pred. No. 1.1e-62;
0; Mismatches 1; Indels (
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Best Local Similarity 99.2%;
Matches 122; Conservative
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, ORGANISM: HUMAN PSCA (hPSCA)
US-10-224-720-6
ORGANISM: HUMAN PSCA (hPSCA)
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Best Local Similarity 99.2
Matches 122; Conservative
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NAME/KEY: SITE
LOCATION: (50)..(64)
FEATURE:
NAME/KEY: SITE
LOCATION: (71)..(82)
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; LOCATION: (67)
US-10-224-720-2
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Search completed: August 18, 2003, 19:52:57 Job time : 55 secs 121 GQL 123 ||| 121 GQL 123 a & a

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GQL 123
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NAME/KEY: SITE
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(cgn2_6/ptodata/1/iaa/BCOMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

(cgn2_6/ptodata/1/iaa/backfiles1.pep:*
        GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-318-503-5
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Maximum Match 100%
Listing first 45 summaries
                                            OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Perfect score:
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Sequence 2, Application US/09203939
GENERAL INFORMATION:
APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Owen N.
TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF.
FILE REPERBUCE: 30435.54US11
CURRENT APPLICATION NUMBER: US/09/203,939
CURRENT APPLICATION NUMBER: 08/814,279
PRIOR APPLICATION NUMBER: 06/011,141
PRIOR PILING DATE: 1999-01-12
PRIOR PLING DATE: 1999-01-12
PRIOR PLING DATE: 1998-01-13
PRIOR FILING DATE: 1998-03-10
PRIOR PLING DATE: 1998-03-10
PRIOR PLING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/074,675
PRIOR APPLICATION NUMBER: 60/034,675
PRIOR APPLICATION NUMBER: 09/038,261
PRIOR PLING DATE: 1998-03-10
SPROWARE: PREMEIN VET: 2.0
SOFTWARE: PREMEIN VET: 2.0
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                                                             US-08-675-508-5
US-08-746-397-11
US-09-27-357-238
US-08-154-916-3
US-08-148-561-1
US-08-448-561-1
US-09-300-584-4
US-08-300-584-4
US-08-476-123-4
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US-08-459-009-12
US-08-459-951-12
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ORGANISM: HUMAN PSCA (hPSCA)
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NAME/KEY: SITE
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NAME/KEY: SITE
LOCATION: (67)..(81)
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ORGANISM: HUMAN PSCA (hPSCA)
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Matches 122, Conservative
; NAME/KEY: SITE
; LOCATION: (50)...(64)
; NAME/KEY: SITE
; LOCATION: (71)...(82)
; NAME/KEX: SITE
; LOCATION: (67)...(81)
US-09-251-835-2
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US-09-318-503-2
                                                                                                                                                                                                 Query Match
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                                                             Sequence 6, Application US/09203939
; Sequence 6, Application US/09203939
; Fatent No. 6258939
; GENERAL INFORMATION:
; APPLICANT: Reiter, Owen N.
; TITLE OF INVENTION:
; FILE REPERENCE: 30435.541051
; CURRENT APPLICATION NUMBER: US/09/203,939
; CURRENT FILING DATE: 2000-12-02
; PRIOR APPLICATION NUMBER: 08/09/1,141
PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR FILING DATE: 1998-01-12
; PRIOR FILING DATE: 1998-02-33
; PRIOR FILING DATE: 1998-03-10
; PRIOR FILING DATE: 1998-03-10
; PRIOR PLING DATE: 1998-03-10
; SEQ ID NOS: 16
; SEQ ID NOS: 16
; SEQ ID NOS: 16
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Pred. No. 5.1e-68;
0; Mismatches 1; Indels
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TITLE OF INVENTION: PSCA.
TITLE OF INVENTION: PSCA.
FILTE OF INVENTION: PSCA.
FILTE OF INVENTION: PSCA.
FILTE OF INVENTION: PSCA.
CURRENT APPLICATION NUMBER: US/09/251, 835A
CURRENT FILING DATE: 1999-02-17
PRIOR PPLICATION NUMBER: 06/071,141
PRIOR FILING DATE: 1997-03-10
PRIOR FILING DATE: 1997-01-12
PRIOR PPLICATION NUMBER: 60/071,141
PRIOR APPLICATION NUMBER: 00/074,675
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR PILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 09/038,261
PRIOR PILING DATE: 1998-12-02
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Best Local Similarity 99.2%;
Matches 122; Conservative
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FEATURE:
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US-09-203-939-6
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SOFTWARE: Patentin Ve
SEQ ID NO 2
LENGTH: 123
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99.8%; Score 645; DB 3; Length 123; 99.2%; Pred. No. 5.1e-68; tive 0; Mismatches 1; Indels
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APPLICANT: Reiter. Robert E.

TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN

FILE REFERENCE: 30435.5401821

CURRENT APPLICATION NUMBER: US/09/251,835A

CURRENT FILING DATE: 1999-02-17

PRIOR PELIOR DATE: 1999-02-17

PRIOR PELIOR DATE: 1999-02-17

PRIOR PELIOR DATE: 1998-01-12

PRIOR PELIOR DATE: 1998-02-13

PRIOR PILING DATE: 1998-02-13

PRIOR PILING DATE: 1998-02-13

PRIOR PILING DATE: 1998-02-13

PRIOR PILING DATE: 1998-02-13

PRIOR PILING DATE: 1998-12-02

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PALENTIN UNEER: 1998-12-02

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PALENTIN UNE: 2.0

SOFTWARE: PALENTIN UNE: 2.0
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EARLIER APPLICATION NUMBER: 09/203,939
EARLIER FILING DATE: 1998-12-02
EARLIER APPLICATION NUMBER: 09/251,835
EARLIER FILING DATE: 1999-02-17
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09038261A Patent No. 6267960
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ORGANISM: HUMAN PSCA (hPSCA)
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US-09-318-503-6
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Best Local Similarity 99.2
Matches 122; Conservative
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; NAME/KEY: SITE
; LOCATION: (71)..(82)
US-09-038-261A-2
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Best Local Similarity
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APPLICANT: Reiter, Robert E.
APPLICANT: Mitch. Owen N.
TILE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
TILE REFERENCE: 30435,540S13
CURRENT PILING DATE: 1999-05-25
EARLIER APPLICATION NUMBER: 08/814,279
EARLIER APPLICATION NUMBER: 08/071,141
EARLIER FILING DATE: 1998-01-12
EARLIER FILING DATE: 1998-01-12
EARLIER FILING DATE: 1998-01-12
EARLIER FILING DATE: 1998-02-15
EARLIER FILING DATE: 1998-02-15
EARLIER FILING DATE: 1998-02-15
EARLIER FILING DATE: 1998-02-15
EARLIER FILING DATE: 1998-02-15
EARLIER FILING DATE: 1998-02-15
EARLIER APPLICATION NUMBER: 60/074,675
EARLIER APPLICATION NUMBER: 60/074,675
                                                                                                       TITLE OF INVENTION: DAGES: PROSTATE STEM CELL ANTIGEN AND USES THEREOF FILE REFERENCE: 30435.540SI3
FILE REFERENCE: 30435.540SI3
CURRENT PELLING NUMBER: US/09/318,503A
CURRENT FILING DATE: 1999-05-25
BARLIER APPLICATION NUMBER: 06/071,141
EARLIER APPLICATION NUMBER: 60/071,141
EARLIER PILING DATE: 1998-01-12
BARLIER FILING DATE: 1998-01-13
EARLIER FILING DATE: 1998-03-10
EARLIER FILING DATE: 1998-03-10
EARLIER PELLON NUMBER: 09/038,261
EARLIER PELLON NUMBER: 09/203,939
EARLIER PELLON NUMBER: 09/203,939
EARLIER FILING DATE: 1998-12-02
EARLIER FILING DATE: 1999-02-17
NUMBER OF SEQ ID NOS: 18
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Pred. No. 5.1e-68;
0; Mismatches 1;
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Patent No. 6261791
Sequence 2, Application US/09318503A
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                                                                   APPLICANT: Reiter, Robert E. APPLICANT: Witte, Owen N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 122; Conservative
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Best Local Similarity
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; LOCATION: (67)..(81)
US-09-318-503-2
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LOCATION: (71)..(82)
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61 VISKGCSLNCVDDSQDYYVGKKNITCCDTDLCNXSGAHALQPAAAILALLPALGLLLWGP 120
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Score 645; DB 3; Length 123;
Pred. No. 5.1e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSTATE STEM CELL ANTIGEN
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APPLICANT: Witte, Owen N.
TITLE OP INVENTION: PSCA. PROSTATE STEM CELL.
FILE REFERENCE: 30435.54USU1
CURRENT APPLICATION NUMBER: US/09/038,261A
CURRENT APPLICATION NUMBER: 08/814,279
PRIOR APPLICATION NUMBER: 08/814,279
PRIOR PILING DATE: 1998-01-12
PRIOR PILING DATE: 1998-01-12
PRIOR PILING DATE: 1998-01-12
PRIOR PILING DATE: 1998-01-12
PRIOR SELING DATE: 1998-01-13
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VET: 2.0
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TYPE: PRT
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APPLICANT: Witte, Owen N.
TITLE OF INVENTION: PSCA.
FILE REFERENCE: 30435.540511
CURRENT APPLICATION NUMBER: US/09/038,261A
CURRENT APPLICATION NUMBER: US/09/038,261A
CURRENT APPLICATION NUMBER: 08/814,279
PRIOR APPLICATION NUMBER: 08/814,279
PRIOR FILING DATE: 1997-03-10
PRIOR FILING DATE: 1998-01-12
PRIOR FILING DATE: 1998-01-13
PRIOR FILING DATE: 1998-02-13
NUMBER: PAPLICATION NUMBER: 60/074,675
PRIOR FILING DATE: 1998-02-13
NUMBER: PATENT DATE: 1998-02-13
NUMBER: PATENT DATE: 1998-02-13
NUMBER: PATENT DATE: 1998-02-13
NUMBER: PATENT DATE: 1998-02-13
NUMBER: PATENT DATE: 1998-02-13
NUMBER: PATENT DATE: 1998-02-13
NUMBER: PATENT DATE: 1998-02-13
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99.2%; Pred. No. 5.1e-68;
iive 0; Mismatches 1
                                                                                          Sequence 6, Application US/09038261A
Patent No. 6267960
                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: HUMAN PSCA (ÅPSCA)
US-09-038-261A-6
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Best Local Similarity 99.29
Matches 122; Conservative
                                                                                                                            GENERAL INFORMATION:
121 GQL 123
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                                                                                 US-09-038-261A-6
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61 VISKGCSLNCVDDSQDYYVGKKNITCCDTDLCNASGAHALQPAAAILALLPALGLLLMGP 120
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APPLICANT: Reiter, Robert E.

APPLICANT: Witte, Owen N.

APPLICANT: Witte, Owen N.

APPLICANT: Witte, Owen N.

APPLICANT: Saffran, Douglas C.

TITLE OF INVENTION: PSCA: PROSTATE STEM CELL ANTIGEN AND USES THEREOF

FILE REPERENCE: 30435.540S14

CURRENT APPLICATION NUMBER: US/09/564,329A

CURRENT APPLICATION NUMBER: 08/359,326

PRIOR PILING DATE: 1999-07-20

PRIOR FILING DATE: 1999-07-20

PRIOR FILING DATE: 1999-07-10

PRIOR FILING DATE: 1998-01-12

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1999-02-13

PRIOR FILING DATE: 1999-02-17

PRIOR APPLICATION NUMBER: 60/113,230

PRIOR PLING DATE: 1999-02-17

PRIOR FILING DATE: 1999-02-17

PRIOR FILING DATE: 1999-02-17

PRIOR FILING DATE: 1999-02-17

PRIOR FILING DATE: 1999-03-16

PRIOR FILING DATE: 1999-03-16

PRIOR FILING DATE: 1999-03-16

PRIOR FILING DATE: 1999-03-16

PRIOR FILING DATE: 1998-13-16

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                   PRIOR APPLICATION NUMBER: 09/203,939
PRIOR FILING DATE: 1998-12-02
PRIOR PLING DATE: 1998-12-02
PRIOR PLING DATE: 1999-02-17
PRIOR PLING DATE: 1999-02-17
PRIOR PLING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 2:
LENGTH: 123
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APPLICATION NUMBER: 09/251,835
FILING DATE: 1999-02-17
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FILING DATE: 1998-03-10
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Matches 122; Conservative
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NAME/KEY: SITE
LOCATION: (71)...(82)
NAME/KEY: SITE
LOCATION: (67)...(81)
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121 GQL 123
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APPLICANT: Au-Young, Janice
TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
TORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.7%; Score 644; DB 2; I
100.0%; Pred. No. 6.7e-68;
iive 0; Mismatches 0;
                                                                                                                                    Score 645; DB 4;
Pred. No. 5.1e-68;
0; Mismatches 1
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SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,508
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08675508
Patent No. 5856136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                      99.8%;
99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM Compatible
                                                                   ; TYPE: PRT
; ORGANISM: HUMAN PSCA (hPSCA)
US-09-564-329A-6
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
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Best Local Similarity 100.
Matches 123; Conservative
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Best Local Similarity 99.2
Matches 122; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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MEDIUM TYPE: Diskette
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1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLT 60

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61 VISKGCSSQCEDDSENYYLGKKNITCCYSDLCNVNGAHTLKPPTTLGLLTVLCSLLLWGS 120
                                                                                      61 VISKGCSLNCVDDSQDYYVGKKNITCCDTDLCNXSGAHALQPAAAILALLPALGLLLMGP 120
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                                                        61 VISKGCSLNCVDDSQDYYVGKKNITCCDTDLCNXSGAHALQPAAAILALLPALGLLLWGP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Reiter, Robert E.
APPLICANT: Witte, Owen N.
TITLE OF INVENTION.
FILE REFERENCE: 30435.54US11
CURRENT APPLICATION NUMBER: US/09/203,939
CURRENT APPLICATION NUMBER: US/09/203,939
CURRENT APPLICATION NUMBER: 08/814,279
PRIOR FILING DATE: 1999-00-112
PRIOR PLING DATE: 1999-01-12
PRIOR PLING DATE: 1999-01-12
PRIOR PLING DATE: 1999-02-13
PRIOR FILING DATE: 1999-02-13
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
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1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLT 60
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APPLICANT: Reiter, Robert E.
APPLICANT: Reiter, Robert E.
APPLICANT: Reiter, Owen N.
1TITLE REFERENCE: 30435.54US12
CURRENT APPLICATION NUMBER: US/09/251,835A
CURRENT FILING DATE: 1999-02-17
PRIOR APPLICATION NUMBER: 08/814,279
PRIOR APPLICATION NUMBER: 60/071,141
PRIOR APPLICATION NUMBER: 60/071,141
PRIOR FILING DATE: 1998-01-12
PRIOR PELLOR DATE: 1998-02-13
PRIOR APPLICATION NUMBER: 60/074,675
PRIOR APPLICATION NUMBER: 09/038,261
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; Pred. No. 6e-38;
16; Mismatches
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Patent No. 6258939
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58.5%;
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; ORGANISM: MURINE PSCA (mPSCA)
US-09-203-939-7
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SEQ ID NO 7
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APPLICANT: Mitte, Owen N.
TITLE OF INVENTION: PEGSTATE STEM CELL ANTIGEN AND USES THEREOF
FILE REFERENCE: 30435.54UG13
CURRENT FILING DATE: 1999-05-25
CURRENT FILING DATE: 1999-05-10
EARLIER APPLICATION NUMBER: 06/071,141
EARLIER FILING DATE: 1998-01-12
EARLIER APPLICATION NUMBER: 60/071,141
EARLIER PILING DATE: 1998-01-13
EARLIER APPLICATION NUMBER: 06/074,675
EARLIER APPLICATION NUMBER: 06/074,675
EARLIER APPLICATION NUMBER: 09/038,261
EARLIER APPLICATION NUMBER: 09/038,261
EARLIER APPLICATION NUMBER: 09/203,939
EARLIER FILING DATE: 1998-03-10
EARLIER FILING DATE: 1998-12-02
EARLIER APPLICATION NUMBER: 09/203,939
EARLIER FILING DATE: 1999-02-17
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN OF: 2.0
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58.5%; Pred. No. 6e-38;
:ive 16; Mismatches 3
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 09/203,939
PRIOR FILING DATE: 1998-12-02
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/09318503A Patent No. 6261791 GENERAL INFORMATION:
                                                                                                                                                               TYPE: PRT
ORGANISM: MURINE PSCA (mPSCA)
US-09-251-835-7
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; ORGANISM: MURINE PSCA (mPSCA)
US-09-318-503-7
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Best Local Similarity 58.5<sup>3</sup>
Matches 72; Conservative
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Peptide epitope 1 PS116 antigen. Ho Peptide epitope 3 Human stem cell an Haematopoietic ste

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Title: Perfect score:

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Prostate stem cell antigen, PSCA; human; prostate cancer; diagnosis; therapy; vaccine; antibody.
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/note= "claimed fragment (Claim 5)"
/note= "claimed fragment (Claim 6)"
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                                                                                                                                                                                             AAY99711
AAW30568
AAB35286
AAU76693
ABB11977
ABP08688
AAW80958
AAW80957
AAW80957
AAW80957
AAW80957
AAW86025
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10-MAR-1997;
12-JAN-1998;
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                                                                                                                                                               August 18, 2003, 19:31:29 ; Search time 85 Seconds (without alignments) 229.687 Million cell updates/sec
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                    Sencore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                       This polypeptide comprises a novel human prostate-specific cell surface antigen (PSCA) that is widely over-expressed across all stages of prostate cancer, including high grade prostate across all intrappithelial neoplasia and androgen-dependent and -independent intrappithelial neoplasia and androgen-dependent and -independent prostate tumours. The amino acid sequence was deduced from isolated cDNA clones (see AAN31861), and contains the highly conserved cysteine residues of the Ly-6/Thy-1 gene family, as well as showing homology to GPI-anchored proteins. PSCA proteins may be used as diagnostic and/or prognostic markers of prostate cancer. PSCA (or encoding nucleic acids) can also be used therapputically in vaccines, in assays to isolate ligands or other binding agents in vaccines antibodies. PSCA antibodies are useful in diagnostic/prognostic assays to detect PSCA, e.g. to diagnose or monitor the progress of prostate cancer in subjects. Claimed immunoconjugates, including an antigen binding region (see AMM70523-24) of the antibody and a toxin agent such as ricin, can be used to selectively kill cells expressing PSCA antigens (claimed) and a toxin agent such as ricin, can be used to selectively kill cells expressing PSCA antigens (claimed) and a loss of producing pSCA protein are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                            New prostate stem cell antigen protein, PSCA - useful in diagnosis and treatment of prostate cancer, e.g. to produce vaccines or generate antibodies for use in assays or therapeutically
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                                                                                                                                                                                           Claim 2; Fig 1B; 63pp; English
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Matches 122, Conservative
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This sequence represents a PS116 antigen. The PS116 gene sequences were isolated as expressed sequence tag (BST) clone of the PS116 gene isolated from a human prostate tissue library. The PS116 sequences can be used in the method of the invention for detecting a target PS116 polynucleotide (PN), that comprises: contacting a sample with at least 1 PS116-specific PN or complement; and detecting the target PS116 polynucleotide (PN), that comprises: contacting the target PS116 polynucleotide (PN), that comprises: contacting the target PS116 polynucleotide (PN), as at least 50% identity with the PS116 sequences. The PNs, PS116 polypeptides (such as this sequence) or PS116 amplicons are used to detect prostate disease. Antibodies (ABs) against PS116 are used to attached to a solid phase. The polypeptides are used for detecting attached to a solid phase. The polypeptides are used for detecting PS116 specific ABs in a sample, and for producing Abs after immunishing subject to obtain Abs. The CDNs and polypeptides are useful for detecting, diagnosing, staging, monitoring, prognosticating, in vivo taging, preventing, treating or determining the predisposition of a subject to diseases and conditions of the prostate, such as prostate enterming the predisposition of a subject the diseases and conditions of the prostate, such as prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 VISKGCSLNCVDDSQDYYVGKKNITCCDTDLCNXSGAHALQPAAAILALLPALGLLWGP 120
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                                                                                                                                                                           New method for detecting diseases of the prostate - comprises use of a PS116 polynucleotide, protein or antibodies, useful for preventing and treating prostate infections and cancer
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monitoring; in vivo imaging; cancer; agonist; antibody; tumour;
metastasis.
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                                                                            Kratochvil JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
99.8%; Score 645; DB 20; Length 123;
Best Local Similarity 99.2%; Pred. No. 2.9e-63;
Matches 122; Conservative 0; Mismatches 1; Indels 0
                                                         Friedman PN
                                                                            MR,
                                                         Cohen M, Colpitts TL,
s EN, Hodges SC, Klass
ussell JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prostate diseases, tumours and metastases
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                                                                                                                                                                                                                                                                  Claim 17; Page 97; 118pp; English
                                                                            Gordon J, Granados EN, Hodg
Roberts-Rapp L, Russell JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                        WPI; 1999-045234/04.
                   (ABBO ) ABBOTT LAB
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                                                         Billing-Medel PA,
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Reiter R, Witte O;
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                                                                                            Misc-difference
 Misc-difference
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                                             Modified-site
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17-FEB-1999;
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                                                                                                                                                                                                                                            from urinary tract tissue. The invention relates to a method of detecting the presence of a target UT116 polynucleotide in a test sample using UT116 gene specific sequences (AAV80136 to AAV80139). Host cells transfected with an expression vector containing the UT116 gene can be used to produce a UT116 polypeptide recombinantly. This polypeptide has at least one UT116 polypeptide recombinantly. This polypeptide has UT116 antigen in a test sample. The polynucleotides and polypeptides are useful for detecting, diagnosing, monitoring, staging, prognosticating, in vivo imaging, preventing, treating or determining the predisposition of a subject to diseases and conditions of the urinary tract, such as urinary tract cancer. Antibodies specifically binding to an epitope of UT116 antigen, and agonists are useful for treating urinary tract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                     represents the consensus sequence of the UT116 polypeptide, derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLT
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                                                                                                                                                              New method for detecting diseases of the urinary tract - comprises use of a UT116 polynucleotide, protein or antibodies, used for preventing and treating urinary tract infections and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, prostate cancer, prostate stem cell antigen, PSCA, chromosome 8q24.2; bladder cancer; anti-apoptosis, proliferation, GPI-anchored cell surface antigen; glycosylphosphatidylinositol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 645; DB 20; Length 123;
Pred. No. 2.9e-63;
0; Mismatches 1; Indels (
                                                                               M, Colpitts TL, Friedman
Klass MR, Kratochvil JD;
JC, Stroupe SD;
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/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                           diseases, tumours and metastases.
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99.2%;
                                                                                          Hodges SC, Kla
, Russell JC,
           98WO-US09972.
                                  97US-0856652
                                                                                Cohen M,
                                                                                                                          WPI; 1999-045237/04.
N-PSDB; AAV80396, AAV$0397.
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Best Local Similarity
Matches 122; Conserva
                                                       (ABBO ) ABBOTT LAB
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                                                                               Billing-medel PA,
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                                                                                                     Roberts-rapp L,
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                                  15-MAY-1997;
                                                                                            Granados EN,
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Peptide
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The present sequence is the human Prostate Stem Cell Antigen (PSCA).

PSCA is a glycosylphosphatidylinositol (GPI)-anchored cell surface antigen, which is expressed across a variety of normal cells: prostate cells, urothelium, renal collecting ducts, colonic neuroendocrine cells, placenta, bladder and ureteral transitional epithelial cells. However, psch is widely over-expressed across all stages of prostate cancer, including high grade prostatic intraeppithelial neoplasia (PIN), androgen-dependent and androgen-independent prostate tumours and bladder carcinoma. The expression of PSCA appears to correlate with increasing grade and so PSCA may be used as a prostate cancer, to discriminate between malignant prostate cancers, normal prostate glands and non-malignant neoplasias. It is hypothesised that PSCA may play a call entipension and or proliferation. The PSCA gene has been localised to chromosome 80434.2. Fragments of the present sequence (AAY99712, AAY99713 and AAY99714) may be used as antigens to produce antibodies grants and prostate cancer. The antibodies may then be used to detect and quantify the presence of PSCA proteins is samples and hence diagnose and prognose prostate cancer. The antibodies may also be used in the treatment of cancers associated with PSCA by inhibiting its expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prostate stem cell antigens, the nucleic acids encoding them and antibodies against them, useful for diagnosing and treating prostate cancer, bladder carcinomas and/or bone metastases of prostate cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100..123
/label= GPI-anchoring_sequence
                                                                                                                                                                                                                                                                                  /note= "Encoded by TTA"
                                                                                                                                                                                                                                                                                                                                                             'note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                             'note= "N-glycosylated"
                                                                                                                                           'note= "N-glycosylated"
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                              21..123
/label= Mature_protein
"Encoded by GTG'
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Best Local Similarity 99.2
Matches 122; Conservative
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The present sequence is human prostate stem cell antigen (PSCA).

PSCA is a single subunit glycoprotein that is expressed on the cell subunit glycoprotein that is expressed on the protein. The present invention relates to anti-PSCA antibody composition and methods of killing PSCA-expressing cancer cells. PSCA is useful for inhibiting and killing the growth of PSCA-expressing cancer cells such as prostate cancer, bladder cancer or lung cancer cells. Humanised antibody cancer cells. PSCA is useful for specifically targetting PSCA-expressing tumour cells in vivo and for inhibiting or killing these cells. The antibodies are also useful for treating the above mentioned cancers and for diagnosing and steging of PSCA-expressing cancer, for purification or immunoprecipitation of PSCA from cells, and for detection and quantitation of PSCA in vitro. PSCA DNA is also useful for treating
61 VISKGCSLNCVDDSQDYYVGKKNITCCDTDLCNASGAHALQPAAAILALLPALGLLLWGP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel anti-prostate stem cell antigen (PSCA) antibody that internalizes on binding to PSCA on mammalian cell and inhibits growth of PSCA-expressing cancer cells in vivo, useful for killing PSCA-expressing cancer cells -
                                                                                                                                                                                                                                                                 Human; prostate stem cell antigen; PSCA; cytostatic; gene therapy; glycoprotein; cancer; prostate; bladder; lung; tumour.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "C-terminal GPI-anchoring sequence"
                                                                                                                                                                                                                                                                                                                                                                               Human prostate stem cell antigen (PSCA) protein.
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                                                                                                                                       AAE03746 standard; Protein; 123 AA
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16-FEB-2000; 2000US-0182872.
                                                                                                                                                                                                   (first entry)
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Best Local Similarity
                              GQL 123
                                                           GQL 123
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                              121
                                                                                                                                                                   AAE03746;
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The present invention relates to new antibodies that specifically bind a novel prostate stem cell antigen (PSCA), which is widely over-expressed across all stages of prostate cancer. The antibodies of the invention are useful to kill tumour cells expressing PSCA and as PSCA expression is observed in prostate tumour cells and in other human cancers, particularly bladder and pancreatic carcinomas, the antibodies are useful therapeutically to treat these diseases. In particular, monoclonal antibodies can be administered to subjects suffering from PSCA-associated
                                                                                                  61 VISKGCSLNCVDDSQDYYVGKKNITCCDTDLCNASGAHALQPAAAILALLFALGLLLMGP 120
                                                                                  VISKGCSLNCVDDSQDYYVGKKNITCCDTDLCNXSGAHALQPAAAILALLPALGLLLWGP 120
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                                                     9
                                           1 MKAVILALIMAGIALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLT
                          1 MKAVILLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLT
                                                                                                                                                                                                                                                                                                                                                         Human; prostate stem cell antigen; PSCA; antibody; immunogen; prostate cancer; bladder cancer; pancreatic cancer; immunoconjugate; PSCA-associated cancer; PSCA antigen.
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                                                                                                                                                                                                                                                                                                                                   Human prostate stem cell antigen (PSCA) protein seguence.
1; Indels
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0; Mismatches
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98US-071141P.
98US-074675P.
99US-11230P.
99US-120536P.
99US-124658P.
98US-033335.
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 Matches 122; Conservative
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SAFFRAN D C.
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02-DEC-1998;
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prostate, bladder or parcreatic cancer, to inhibit the cancer and prolong the subject's life. The antibodies can be combined with a therapeutic agent in immunoconjugates useful to treat subjects suffering from malignant diseases, characterised by cells having PSCA antigen on the cell surface e.g. cancers, by killing the cells. The antibodies and immunoconjugates may also be included with a carrier in pharmaceutical compositions useful to kill human cells expressing PSCA antigen on the cell surface. The antibodies are also useful diagnostically to detect cancer, especially prostate cancer, to isolate prostate cancer cells compounds, assist in identification of rare genes associated with prostate cancer, and to isolate and purify PSCA and PSCA homologues.

The present amino acid sequence represents the human prostate stem cells antigen (PSCA) protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                     Gaps
 e.g. prostate, bladder or pancreatic cancer or metastatic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human bladder cancer associated protein sequence SEQ ID NO:169.
                                                                                                                                                                                                                                                                                                             99.8%; Score 645; DB 23; Length 123; 99.2%; Pred. No. 2.9e-63; ive 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; bladder cancer; cytostatic; gene therapy; vaccine
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13-NOV-2001; 2001US-35066FP.
12-APR-2002; 2002US-372246P.
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2001US-310099P.
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Matches 122; Conservative
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N-PSDB; ACC51040.
                                                                                                                                                                                                                                                                             123 AA;
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The present invention describes a method for detecting a bladder cancerassociated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is 80 % identical to a table of sequences (see ACC50951 to ACC5095). ACC50951 to ACC51059 trable of sequences cancer-associated proteins given in ABR48146 to ABR48342). Bladder cancer-associated sequences from the present invention have cytostatic activities, and can be used for detecting a bladder cancer-associated transcript in a cell from a patient. The method can be used for detecting a bladder cancer-associated transcript in a cell from a patient. The method is useful in diagnosing or treating bladder cancer and in screening for compounds that modulate bladder cancer, and is screening for the nucleic acid molecules from the present invention may be used in various screening and diagnostic methods, and for gene therapy, vaccine
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                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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Pred. No. 2.9e-63;
0; Mismatches 1; Indels C
                                                                                                                                                                                                                                                             and/or antisense/inhibition applications
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Best Local Similarity 99.2%;
Matches 122; Conservative (
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N-PSDB; ABQ83853.
                                                                                                                                                                                                                                                                                                  123 AA;
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The present invention describes an isolated epitope (I) and an epitope cluster. Also described is a vaccine or immunotherapeutic composition (VC) comprising (I). (I) has cytostatic activity. VC is useful for treating an animal, by administering to an animal the vaccine or immunotherapeutic composition. VC is also useful for evaluating immunotherapeutic composition. VC is also useful for evaluating camposition, by administering VC to an HLA-transgenic animal and evaluating immunogenicity based on a characteristic of the animal, or by in vitro primary stimulation of a T cell and evaluating immunogenicity. (I) is useful for determining specific T cell frequency, by contacting T cells with a MHC-peptide complex, and further comprises ELISPOT analysis, complimiting dilution analysis, flow cytometry, in situ hybridisation and/or polymerase chain reaction (PCR). ABQ83843 to ABQ83858 and ABP74128 to the ABP7413 represent sequences used in the exemplification of the present
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Pred. No. 2.9e-63;
0; Mismatches 1; Indels C
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|label= SCAH-2
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Best Local Similarity 99.2%;
Matches 122; Conservative C
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N-PSDB; AAV38045.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention.
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The present sequence represents human stem cell antigen 2 (SCAH-2). SCAH proteins can be administered therapeutically, e.g. to inhibit or reverse the development of tumours. Antibodies to SCAH proteins can be used in diagnostic tests for conditions associated with protein expression in bological samples, by combining a sample with the antibody under conditions suitable for antibody binding to the protein to form a complex, and detecting the complex. Antibodies to SCAH-2 are especially useful in diagnostic tests for conditions such as leukaemias or malignant local tumours associated with SCAH-2 expression. SCAH-1 and SCAH-2 have homology to Sca-2 and other stem cell antigens, and have characteristics of the LV-6 family of cysteine rich proteins. The functional similarities among LV-6 family proteins previously reported, and the expression of SCAH-1 and SCAH-2 in tumours from several tissues (e.g. breast, lung, bladder) indicated that SCAH proteins may be useful as anticancer agents; SCAH antibodies, antagonists or inhibitors indicated using the proteins could also be useful in anticancer receiption and autoimmune diseases e.g. lupus nephritis. The nucleic acid sequences encoding SCAH proteins are also useful therapeutically to rejection and autoimmune diseases e.g. lupus nephritis. The nucleic acid sequences encoding SCAH proteins are also useful therapeutically to treat, e.g. leukaemias and cancers of the bladder or breast.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 VISKGCSLNCVDDSQDYYVGKKNITCCDTDLCNXSGAHALQPAAAILALLPALGLLLWGP
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0
Human stem cell antigens, SCAH-1 and SCAH-2 - useful to, e.g. diagnose and treat SCAH-1 or SCAH-2 related conditions such as tumours and screen inhibitory compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.7%; Score 644; DB 19;
100.0%; Pred. No. 3.8e-63;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY13938 standard; Protein; 123 AA
                                                                                Claim 16; Fig 2; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PROT-) PROTEGENE INC. (SAGA ) SAGAMI CHEM RES CENT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9918203-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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WPI; 2001-159478/16.
N-PSDB; AAF27971.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                      61 VISKGCSLNCVDDSQDYYVGKKNITCCDTDLCNXSGAHALQPAAAILALLPALGLLLWGP 120
                                                                                                             All of the proteins exist in the cell membrane, so are considered to be proteins controlling the proliferation and differentiation of the cells. They may be useful as carcinostatic agents or as antigens for preparing antibodies against the proteins. The CDNAs can be used as probes for gene diagnosis and gene sources for gene therapy, as well as for protein may be associated with signal transduction associated with spoptosis, and therefore useful in inhibition of apoptosis. The HP01962 (see AAY13943) protein can be used to treat diseases associated with phopshatidlethanolamine N-methyltransferase. The proteins are identified by the presence of a hydrophobic transmembrane region, knowledge of the protein is not required, as in e.g. methods of
                                                                                                                                                                                                                                                                                                                                          1 MKAVLIALIMAGLALQPGTALLCYSCKAQVSNEDCLQVKNCTQLGEQCWTARIRAVGLIT 60
                                                                                                                                                                                                                                                                                                                              1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLT
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prostate stem cell antigen; PSCA; human; mouse; prostate cancer; diagnosis; treatment; chromosome 8q24.2.
                                                                                                      sequence is a human transmembrane protein of the invention.
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                                                                                                                                                                                                                                                                                    Length 123;
                                                                                                                                                                                                                                                                                                          1; Indels
                                                             Human transmembrane proteins and nucleotide sequences
                                                                                                                                                                                                                                                                                   99.2%; Score 641; DB 20; 98.4%; Pred. No. 8.1e-63; ive 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saffran DC, Jakobovits A;
          Yamaguchi
                                                                                  Claim 1; Page 82-83; 139pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB35285 standard; Protein; 123 AA
          Sekine S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human prostate stem cell antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUL-1999; 99US-0359326.
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                                         N-PSDB; AAX36800, AAX36801.
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Matches 121; Conservative
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          Kobayashi M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reiter R, Witte O,
                              WPI; 1999-277268/23
                                                                                                                                                                                                                                                                 123 AA;
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                                                                                                                                                                                                                                                                 Sequence
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          Kato S,
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The present invention describes a method of treating cancer associated with prostate stem cell antigen (PSCA) by administering an antibody which selectively binds to PSCA and inhibits the growth of the cancer cells. The PSCA gene is found on human chromosome 8q24.2. The invention provides the human and murine PSCA protein and coding sequences, which can be used not only in the treatment of, but also in detection and prognosis of prostate cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MNAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLT 60
Antibodies binding to prostate stem cell antigen inhibit the growth of cancer cells and are used to detect and treat prostate, pancreatic or bladder cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, PRO; benign tumour; malignant tumour; lymphoid malignancy;
leukaemia; neuronal disorder; stromal disorder; blastocoelic disorder;
inflammatory disorder; immune disorder; angiogenic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKAVILIALIMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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Pred. No. 1e-62;
0; Mismatches 2; Indels (
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                                                                                                                      Example 1; Fig 1B; 229pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.1%;
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990S-133459P.
990S-140650P.
990S-140653P.
990S-14063P.
990S-145698P.
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99US-151689P.
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99WO-US28313
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Best Local Similarity 98.4
Matches 121, Conservative
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5 LLALLMAGLALOPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLTVISK 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                       65 GCSLNCVDDSQDYYVGKKNITCCDTDLCNXSGAHALQPAAAILALLPALGLLLWGPGQL 123
                                                                                                                                                                                                      polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, agonists, antegonists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic, glandular, and angiogenic disorders. The polynucleotide sequences are also useful in gene therapy. Augs6128-AAU86162 represent the human PRO polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secreted protein; transmembrane protein; human; enterocolitis; Zollinger-Ellison syndrome; gastrointestinal ulceration; congenital microvilus atrophy; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease; Alshaimer's disease; Als, neuropathy; fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;
                                                                                                                                                                                                   The present invention relates to the isolation of novel human PRO
                                                                                                                                     Thirty five nucleic acids encoding PRO polypeptides, useful for treating benign or malignant tumours, leukaemias and lymphoid malignancies, inflammatory, angiogenic and immunologic disorders
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                                                             Hillan KJ;
Stone DM;
                                                                                                                                                                                                                                                                                                                                        97.1%; Score 627; DB 23; Length 119; 99.2%; Pred. No. 2.7e-61; ive 0; Mismatches 1; Indels (
                                                              Gurney AL,
Smith V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  anti-thrombotic; wound healing; tissue repair
                                                             d A, Godowski PJ, C
Pitti RM, Roy MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of protein PRO232.
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                                                                                                                                                                               Claim 61; Fig 8; 302pp; English.
         01-DEC-1999; 99WO-US28634.
05-JAN-2000; 2000WO-US00219.
99WO-US28301.
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97US-0059113.
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                                                             Goddard A,
                                                                                                                                                                                                                                                                                                                                                             Matches 118; Conservative
                                                                       Marsters SA, Pan J, I
Watanabe CK, Wood WI;
                                         (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                       2002-205567/26.
                                                                                                                                                                                                                                                                                                                     Sequence 119 AA;
                                                                                                                N-PSDB; ABK40257
                                                              Ashkenazi AJ,
 01-DEC-1999;
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17-SEP-1997;
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ID AAY1
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AAY13344-403 represent secreted and transmembrane human proteins. The CDNA sequences are obtained from CDNA libraries, prepared from fetal lung, fetal skidney, fetal brain, fetal liver and fetal retina. The encoded polypeptides have specific uses based on their homology to known polypeptides, e.g. PRO211 and PRO217 can be used for disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions and the repair of acute and chronic mucosal lesions ulceration ulceration and congenital microvillus atrophy, skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of the vulva and gliomas), potent effects on cell growth and development, diseases related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated human genes and polypeptides used in, e.g. treatment of gastrointestinal ulceration
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970S-0059121.
970S-0059122.
970S-0059184.
970S-0059263.
970S-0059266.
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97US-0063121.
97US-0063127.
97US-0063128.
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97US-0063327.
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970S-0063564.
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970S-0063732.
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97US-0062814.
97US-0062816.
97US-0063045.
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97US-0063549.
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97US-0063870.
97US-0064103.
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97US-0064809.
97US-0065186.
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97US-0066453
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29-OCT-1997;
29-OCT-1997;
29-OCT-1997;
29-OCT-1997;
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24-0CT-1
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Novel anti-prostate stem cell antigen (PSCA) antibody that internalizes
cell surface as a glycosylphosphatidylinositol
                                                                                                                                                                                                                                                                                                                                                        92.9%;
93.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-OCT-1999; 99US-0162558.
16-FEB-2000; 2000US-0182872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH ) GENENTECH INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Keller G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-389954/41.
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 115; Conserv
                                                                                                                                                                                                                                                                                                                123 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAD08174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAE03758
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                                                                                                                                                                                                                                                                                                                                                             10 MAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLTVISKGCSLN 69
                                                                                                                                                                                                                                                                                                                                                                                    1 MAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLTVISKGCSLN 60
                Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used as a target for anti-tunor drugs. PRO533 may be used in the treatment of Usher Syndrome or Atrophia areata; PRO569 can be used as an anti-thrombotic agent; PRO287 polypeptides and portions may have therapeutic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endomecrium, blood vessels, or related tissue, e.g. in the heart of genital tract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel anti-prostate stem cell antigen (PSCA) antibody that internalizes on binding to PSCA on mammalian cell and inhibits growth of PSCA-expressing cancer cells in vivo, useful for killing PSCA-expressing cancer cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is cynomolgus (monkey) type II prostate stem cell antigen (PSCA). PSCA is a single subunit glycoprotein that is expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cynomolgus (monkey) type II prostate stem cell antigen (PSCA) protein.
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 CVDDSQDYYVGKKNITCCDTDLCNXSGAHALQPAAAILALLPALGLLLWGPGQL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CVDDSQDYYVGKKNITCCDTDLCNASGAHALQPAAAILLALLPALGILLWGPGQL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monkey; prostate stem cell antigen; PSCA; cytostatic; gene therapy;
glycoprotein; cancer; prostate; bladder; lung; tumour.
  growth or survival of nerve cells including Parkinson's disease,
                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                               94.0%; Score 607; DB 20; Length 114; 99.1%; Pred. No. 4.1e-59; ive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "C-terminal GPI-anchoring sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE03759 standard; Protein; 123 AA
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                                                                                                                                                                                                                                                                                    Best Local Similarity 99.1%;
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-OCT-1999; 99US-0162558.
16-FEB-2000; 2000US-0182872.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macaca fascicularis.
                                                                                                                                                                                                                          114 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE03759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
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61 VISKGCSLNCVDDSQDYYVGKKNITCCDTDLCNXSGAHALQPAAAILALLPALGLLLWGP 120
                  protein. The present invention relates to anti-BSCA antibody composition and methods of killing PSCA-expressing cancer cells. PSCA is useful for inhibiting and killing the growth of PSCA-expressing cancer cells such as prostate cancer, bladder cancer or lung cancer cells. Humanised antibody conjugated to a toxin or a radioactive isotope is used for killing the cancer cells. PSCA is useful for specifically targetting PSCA-expressing tumour cells in vivo and for inhibiting or killing these cells. The antibodies are also useful for treating the above mentioned cancers and for diagnosing and staging of PSCA-expressing cancer, for purification or immunoprecipitation of PSCA from cells, and for detection and quantitation of PSCA in vitro. PSCA DNA is also useful for treating cancers by gene therapy techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLNVENCTQPEEQCWTERIRAVGLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cynomolgus (monkey) type I prostate stem cell antigen (PSCA) protein
(GPI) -anchored
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monkey; prostate stem cell antigen; PSCA; cytostatic; gene therapy; glycoprotein; cancer; prostate; bladder; lung; tumour.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "C-terminal GPI-anchoring sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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/label= Mature_typeI_PSCA_protein
21..100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 600; DB 22;
Pred. No. 2.7e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lasky LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE03758 standard; Protein; 123 AA.
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The present sequence is cynomolgus (monkey) type I prostate stem cell antigen (PSCA). PSCA is a single subunit glycoprotein that is expressed on the cell surface as a glycosylphosphatidylinositol (GPI)—anchored protein. The present invention relates to anti-PSCA antibody composition and methods of killing PSCA-expressing cancer cells. PSCA is useful for inhibiting and killing the growth of PSCA-expressing cancer cells such as prostate cancer or lung cancer cells. Humanised antibody conjugated to a toxin or a radioactive isotope is used for killing the conjugated to a toxin or a radioactive isotope is used for killing the cancer cells in vivo and for inhibiting the above mentioned cancers and for inhibiting the above mentioned cancers and for immunopracipitation of PSCA-expressing cancer, for purification of or immunopracipitation of PSCA from cells, and for detection and quantitation of PSCA from cells, and for detection and quantitation of pSCA humines.
on binding to PSCA on mammalian cell and inhibits growth of PSCA-expressing cancer cells in vivo, useful for killing PSCA-expressing cancer cells -
                                                                                                             Example 6; Fig 15; 112pp; English.
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Query Match
Best Local Similarity 92.7
Matches 114; Conservative 123 AA; Sequence

1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLNVENCTQPEEQCWTERIRAVGLLT 60 1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLT 60 0; Gaps 92.0%; Score 594; DB 22; Length 123; 92.7%; Pred. No. 1.2e-57; ive 0; Mismatches 9; Indels C

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61 VISKGCSLNCVDDSQDYYVGKKKNITCCDTDLCNXSGAHALQPAAAILALLPALGLLLWGP 120

121 GQL 123

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121 ROL 123

Search completed: August 18, 2003, 19:41:26 Job time : 86 secs

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMAKIES	•
		dР				
Result No.	Score	Query Match	Query re Match Length DB	DB	. qi	Description
-	122	66	125	- 6	•	Human stem cell an
10	693	75.6	. 123	61	AAW70522	Human prostate ste
m	93	75.6		20	AAW80956	PS116 antigen. Ho
4	93	75.6		20	AAW86024	UT116 polypeptide
'n	93	75.6		21	AAY99707	Human prostate ste
9	93	75.6		22	AAE03746	Human prostate ste
7	93	75.6		23	AAU76692	Human prostate ste
8	93	75.6		24	ABR48224	Human bladder canc
σ	93	75.6		24	ABP74203	Human PSCA protein

(INCY-) INCYTE PHARM INC.

ä	PR0232	Amino acid sequenc	Human transmembran	stem cell	antigen.	Peptide epitope 2	Human 5' EST secre	Human secreted pro	Cynomolgus (monkey	Cynomolgus (monkey	gen.		gen.	oitope	antigen.	Peptide epitope 3	n prostate	prostate	rostate st	e stem	E	prostate	prostate		ORFX	Human PSCA epitope	Human PSCA epitope	Human PSCA epitope	Human PSCA epitope	Human PSCA epitope	prostate	Murine prostate st	e prostate s	tate	e st
AAB35285	AAU86131	AAY13347	AAY13938	ABB11977 .	AAW80958	AAW86026	AAY11900	AAG00606	AAE03758	AAE03759	AAW80957	AAW86025	AAW80960	AAW86028	AAW80959	AAW86027	AAW70523		AAY99714	528	AAB35284	AAW70524	AAY99713	AAB35283	ABP08688	ABP74340	ABP74342	ABP74339	ABP74341	ABP74338	AAW30568	AAY99708	971	AAB35286	99
22	23	20	20	22	50	20	20	21	22	22	20	20	20	20	20	20	19	21	21	22	22	19	21	22	23	24	24	24	24	24	19	21	21	22	23
123	119	114	123	117	41	41	88	88	123	123	34	34	24	24	30	30	15	15	12	15	15	12	12	12	85	10	10	σ	σ	8	123	123	123	123	123
74.0	72.4	68.3		41.5	ω.	ω.	ъ.	33.3	9	29.3	7.	7.	6.	φ.	19.5	φ.	ά.	•								•	٠		7.3	•	6.5	6.5	6.5	•	•
91	8	84	54	51	41	41	41	41	36	36	34	34	24	24	24	. 24	15	15	. 15	15	15	12	12	12	11	10	10	σ	σ	80	œ	80	œ	80	6 0
10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

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Human, stem cell antigen, SCAH-1, SCAH-2, THP-1, bladder tumour; diagnosis, screening, sca-2, LY-6 family; leukaemia, cancer.
                                                                                                                                                   /label= unknown
/note= "encoded by GSC"
                                                                                                                   Location/Qualifiers
       AAW62066 standard; Protein; 125 AA.
                                                                                                                             3..125
/label= SCAH-2
                                                                                                                                                                                                                97WO-US10956
                                                                                                                                                                                                                                 96US-0675508
                                         14-SEP-1998 (first entry)
                                                          Human stem cell antigen 2.
                                                                                                                                             Misc-difference 96
                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                 03-JUL-1996;
                                                                                                                                                                                                                25-JUN-1997;
                                                                                                                                                                              WO9800540-A1
                                                                                                                                                                                               08-JAN-1998
                        AAW62066;
                                                                                                                             Protein
4AW62066
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Matches
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                                                                                                                                                The present sequence represents human stem cell antigen 2 (SCAH-2). SCAH proteins can be administered therapeutically, e.g. to inhibit or reverse the development of tumours. Antibodies to SCAH proteins can be used in diagnostic tests for conditions associated with protein cap be used in biological samples, by combining a sample with the antibody under conditions suitable for antibody binding to the protein to form a complex, and detecting the complex. Antibodies to SCAH-2 are especially useful in diagnostic tests for conditions/diseases such as leukaemias or malignant local tumours associated with SCAH-2 expression. SCAH-1 and SCAH-2 have homology to Sca-2 and other stem cell antigens, and have characteristics of the LV-6 family proteins previously reported, and the expression of SCAH-1 and SCAH-2 in tumours from several tissues (e.g. breast, lung, bladder) indicated that SCAH proteins may be useful as anticancer agents; SCAH antibodies, antigoniers or inhibitors identified using the proteins could also be useful in anticancer criection and autoimmune diseases e.g. lungs nephritis. The nucleic acid sequences encoding SCAH partiboses or jupus nephritis. The nucleic acid sequences encoding SCAH partiboses or jupus nephritis. The nucleic acid sequences encoding SCAH partiboses or jupus nephritis. The nucleic acid sequences encoding SCAH partiboses or jupus nephritis. The nucleic acid sequences encoding SCAH proteins are also useful therapeutically to treat, e.g. leukaemias and cancers of the bladder or breast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 VISKGCSLNCVDDSQDYYVGKKNITCCDTDLCNXSCAHALQPAAAILALLPALGLLLWGP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 VISKGCSLNCVDDSQDYYVGKKNITCCDTDLCNXSGAHALQPAAAILALLPALGILLEWGP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 MKAVILLALIMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLT 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                   Human stem cell antigens, SCAH-1 and SCAH-2 - useful to, e.g. diagnose and treat SCAH-1 or SCAH-2 related conditions such as tumours and screen inhibitory compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prostate stem cell antigen; PSCA; human; prostate cancer; diagnosis; therapy; vaccine; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.2%; Score 122; DB
100.0%; Pred. No. 6.5
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human prostate stem cell antigen (PSCA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW70522 standard; Protein; 123 AA.
                                                                                                                             Claim 16; Fig 2; 66pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 123; Conservative
                            1998-427478/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 AA;
                                         N-PSDB; AAV38045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GQL 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
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AAW70522
ID AAW7
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surface antigen (PSCA) that is widely over-expressed across all stages of prostate cancer, including high grade prostate intraepithelial neoplasia and antorgen-dependent and independent prostate tumours. The amino acid sequence was deduced from prostate tumours. The amino acid sequence was deduced from isolated cDNA clones (see AAV33691), and contains the highly conserved cysteine residues of the Ly-6/Thy-1 gene family, as well as showing homology to GPI-anchored process. PSCA proteins may be used as diagnostic and/or prognostic markers of prostate cancer. PSCA (or encoding nucleic acids) can also be used therapeutically in vaccines, in assays to isolate ligands or other binding agents of and to produce antibodies. PSCA antibodies are useful in diagnostic/prognostic assays to detect PSCA, e.g. to diagnose or monitor the progress of prostate cancer in subjects. Claimed immunoconjugates, including an antigen binding region (see AAV70523-24) of the antibody and a toxin agent such as ricin, can be used to selectively kill cells expressing PSCA antigens (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, expressed sequence tag, EST; prostate disease, diagnosis, tumour; detection, therapy, prostate cancer, metastasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New prostate stem cell antigen protein, PSCA - useful in diagnosis and treatment of prostate cancer, e.g. to produce vaccines or generate antibodies for use in assays or therapeutically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide comprises a novel human prostate-specific cell
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100.0%; Pred. No. 1.2e-79;
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                                                                                                                          98US-0074675.
97US-0814279.
98US-0071141.
                                                              98WO-US04665.
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1es 93; Conservative
                                                                                                                                                                                                                                                                  (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-520801/44.
                                                                                                                                                                                                                                                                                                                                        Reiter R, Witte O;
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                                                              10-MAR-1998;
                                                                                                                                                             10-MAR-1997;
12-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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17-SEP-1998
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Friedman PN;

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This represents the consensus sequence of the UT116 polypeptide, derived derow urinary tract tissue. The invention relates to a method of detecting the presence of a target UT116 polynucleotide in a test sample using UT116 gene-specific sequences (AAV80386 to AAV80397). Host cells transfected with an expression vector containing the UT116 gene can be used to produce a UT116 polypeptide recombinantly. This polypeptide has at least one UT116 epitope which can be used in a method for detecting UT116 antigen in a test sample. The polynucleotides and polypeptides are useful for detecting, ingenorating, reacting, monitoring, steaging, prognosticating, in vivo imaging, preventing, treating or determining the predisposition of a subject to diseases and conditions of the urinary tract, such as urinary tract cancer. Antibodies specifically binding to an epitope of UT116 antigen, and agonists are useful for treating urinary tract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New method for detecting diseases of the urinary tract - cor
use of a UT116 polynucleotide, protein or antibodies, used i
preventing and treating urinary tract infections and cancer

    Colpitts TL, Friedman
Klass MR, Kratochvil JD;

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ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                              Stroupe SD;
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/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Page 94; 113pp; English
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Roberts-rapp L, Russell JC,
                                                                                             98WO-US09972.
                                                                                                                                                        97US-0856652
                                                                                                                                                                                                                                                                                            Billing-medel PA, Cohen M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAV80396, AAV80397.
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                                                                                                                                                                                                                          (ABBO ) ABBOTT LAB
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                                                                                             15-MAY-1998;
                                                                                                                                                               15-MAY-1997;
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                               19-NOV-1998.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a PS116 antigen. The PS116 gene sequences were isolated as expressed sequence tag (EST) clone of the PS116 gene isolated from a human protectet tissue library. The PS116 sequences can be used in the method of the invention of detecting a target PS116 polymucleotide (PN), that comprises: contacting a sample with at least 1 PS116-specific PN or complement; and detecting the target PS116 pN, where the specific PN has at least 50% identity with the PS116 samplesones. The PNs, PS116 polypeptides (such as this sequence) or PS116 amplicons are used to detect prostate disease. Antibodies (Abs) against PS116 are used in assay kits to detect prostate disease. Antibodies (Abs) and the Abs are preferably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 attached to a solid phase. The polypepides are used for detecting PS116-specific Abs in a sample, and for producing Abs after immunising a subject. Plasmids encoding PS116 epitopes can also be administered to a subject to obtain Abs. The coNAs and polypepides are useful for detecting, diagnosing, staging, monitoring, prognosticating, in vivo imaging, preventing, treating or determining the predisposition of a subject to diseases and conditions of the prostate, such as prostate cancer. The Abs and agonists or inhibitors are useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New method for detecting diseases of the prostate - comprises use of a PS116 polynucleotide, protein or antibodies, useful for preventing and treating prostate infections and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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vivo imaging; cancer; agonist; antibody; tumour;
                                                                                                                                                                                                                                                                                            Cohen M, Colpitts TL, Friedman PN;
B EN, Hodges SC, Klass MR, Kratochvil JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 93; DB 20; I
Pred. No. 1.2e-79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.6%; Scc. No. 1.100.0%; Pred. No. 1.100.0%; 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prostate diseases, tumours and metastases.
                                                                                                                                                                                                                                                                                                                               Gordon J, Granados EN, Hodges SC, Klas
Roberts-Rapp L, Russell JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UT116 polypeptide consensus sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 17; Page 97; 118pp; English
                                                                                             98WO-US10041
                                                                                                                                                        97US-0856653
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93; Conservative
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                                                                                                                                                                                                                          (ABBO ) ABBOTT LAB.
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monitoring; in
                                                                                             15-MAY-1998;
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                                                                                                                                                        15-MAY-1997;
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Sequence

Query Match Local Matches

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AAW8602 RESULT

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Gaps

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Length 123; Indels

DB 20; Le 1.2e-79; thes 0;

93 93

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Human; prostate stem cell antigen; PSCA; cytostatic; gene therapy; glycoprotein; cancer; prostate; bladder; lung; tumour.

Homo sapiens

Peptide Protein

Human prostate stem cell antigen (PSCA) protein.

07-AUG-2001

AAE03746;

AAE03746 standard; Protein; 123 AA.

RESULT 6 AAE03746 "C-terminal GPI-anchoring sequence"

/note=

Region

WO200140309-A2

07-JUN-2001

27-OCT-2000; 2000WO-US29603. 29-OCT-1999; 99US-0162558. 16-FEB-2000; 2000US-0182872.

(GETH) GENENTECH INC.

21..123 /label= Mature_human_PSCA_protein 21..100

1..20 /label= Signal_peptide Location/Qualifiers

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The present sequence is the human Prostate Stem Cell Antigen (PSCA).

PSCA is a glycosylphosphatidylinositol (GPI)-anchored cell surface
antigen, which is expressed across a variety of normal cells; prostate
cells, urothelium, renal collecting ducts, colonic neuroendocrine cells,
placenta, bladder and ureteral transitional epithelial cells. However,
pscA is widaly over-expressed across all stages of prostate cancer,
including high grade prostatic intraepithelial neoplasia (PIN),
androgen-dependent and androgen-independent prostate tumours and bladder
carcinoma. The expression of FSCA appears to correlate with increasing
grade and so PSCA may be used as a prostate cancer marker, to
discriminate between malignant prostate cancers, normal prostate glands
and non-malignant neoplasias. It is-hypothesised that PSCA may play a
role in stem/progenitor cell function such as self-renewal
corromosome 8024.2. Fragments of the present sequence (AAN99712,
AAY99713 and AAX99714) may be used as antigens to produce antibodies
against PSCA. The antibodies may then be used to detect and quantify the
prostate cancer. The antibodies may also be used in the treatment of
cancers associated with PSCA by inhibiting its expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prostate stem cell antigens, the nucleic acids encoding them and antibodies against them, useful for diagnosing and treating prostate cancer, bladder carcinomas and/or bone metastases of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                        100..123
/label= GPI-anchoring_sequence
                                                                                     'note= "N-glycosylated"
                                                                                                                     note= "Encoded by TTA"
                                                                                                                                                       'note= "N-glycosylated"
                                                                                                                                                                                      /note= "N-glycosylated"
21..123
/label= Mature_protein
                                                   note= "N-glycosylated'
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99US-0251835.
99US-0318503.
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Matches 93, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-412305/35.
N-PSDB; AAA48374.
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25-MAY-1999;
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The present sequence is human prostate stem cell antigen (PSCA). PSCA is a single subunit glycoprotein that is expressed on the cell surface as a glycosylphosphatidyinositol (GPI)-anchored protein. The present invention relates to anti-PSCA antibody composition and methods of killing PSCA-expressing cancer cells. PSCA is useful for inhibiting and killing the growth of PSCA-expressing cancer cells such as prostate cancer, bladder cancer or lung cancer cells. Humanised antibody conjugated to a toxin or a radioactive isotope is used for killing the cancer cells. PSCA is useful for specifically targetting PSCA-expressing tumour cells in vivo and for inhibiting or killing these cells. The antibodies are also useful for treating the above mentioned cancers and cor diagnosing and steging of PSCA-expressing cancer, for purification or immunoprecipitation of PSCA from cells, and for detection and quantitation of PSCA in vitro. PSCA DNA is also useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel anti-prostate stem cell antigen (PSCA) antibody that internalizes on binding to PSCA on mammalian cell and inhibits growth of PSCA-expressing cancer cells in vivo, useful for killing PSCA-expressing cancer cells .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKAVLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGGQCWTARIRAVGLLT
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Best Local Similarity 100.0%; Pred. No. 1.2e-79;
Matches 93; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koeppen H, Lasky LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancers by gene therapy techniques.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B, Keller G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-389954/41.
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VISKGCSLNCVDDSQDYYVGKKNITCCDTDLCN 93 61 VISKGCSLNCVDDSQDYYVGKKNITCCDTDLCN 93

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The present invention relates to new antibodies that specifically bind a novel prostate stem cell antigen (PSCA), which is widely over-expressed across all stages of prostate cancer. The antibodies of the invention care useful to kill tumour cells expressing PSCA and as PSCA expression is observed in prostate tumour cells expressing PSCA and as PSCA expression is particularly bladder and pancreatic carcinomas, the antibodies are useful therapeutically to treat these diseases. In particular, monoclonal cancers, e.g. prostate, bladder or pancreatic cancer or metastatic prostate, bladder or pancreatic cancer, to inhibit the cancer and prolong the subject's life. The antibodies can be combined with a therapeutic agent in immunoconjugates useful to treat subjects suffering from malignant diseases, characterised by cells having PSCA antigen on the cent of the subject of the subject of the subject of the subject of the cancer and prolong malignant diseases, characterised by cells having PSCA antigen on the compositions useful to kill human cells expressing PSCA antigen on the compositions useful to kill human cells expressing PSCA antigen on the cancer and prolong and immunoconjugates are also useful diagnostically to detect
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                                                                                                                                                                                                                                                Human; prostate stem cell antigen; PSCA; antibody; immunogen;
prostate cancer; bladder cancer; pancreatic cancer; immunoconjugate;
PSCA-associated cancer; PSCA antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigen, PSCA, useful as antitumour agents in treatment of prostate, bladder and pancreatic cancer and in prostate cancer diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antibodies specifically binding a novel prostate cell surface
                                                                                                                                                                                                                  Human prostate stem cell antigen (PSCA) protein sequence.
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VISKGCSLNCVDDSQDYYVGKKNITCCDTDLCN
                     VISKGCSLNCVDDSQDYYVGKKNITCCDTDLCN
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                                                                                                                AAU76692 standard; Protein; 123 AA
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98US-074675P.
98US-113230P.
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99US-124658P.
98US-0038261.
98US-0203939.
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99US-0318503.
99US-0359326.
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                                                                                                                                                                                  (first entry)
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SAFFRAN D C.
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                                                                                                                                                                                                                                                                                                                                                        US2001055751-A1.
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21-DEC-1998
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                                                                                                                                                AAU76692;
 63
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(SAFF/)
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                 compounds, assist in identification of rare genes associated with prostate cancer, and to isolate and purify PSCA and PSCA homologues. The present amino acid sequence represents the human prostate stem cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting a bladder cancer-associated transcript in a cell from a patient, comprises contacting a biological sample from the patient with a bladder cancer-associated polynucleotide or antibody
                                                                                                                                                                                                                                      1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLT
                                                                                                                                                                                                                 1 MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLT
                                                                                                                                                                                 Gaps
e.g. to enable culture growth to evaluate candidate therapeutic
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                                                                                                                                             Length 123;
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                                                                                                                                             DB 23; L
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                       61 VISKGCSLNCVDDSQDYYVGKKNITCCDTDLCN
                                                                         antigen (PSCA) protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                      ABR48224 standard; Protein; 123
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2001US-343705P.
2001US-350666P.
2002US-372246P.
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                                                                                                                                                                               93; Conservative
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N-PSDB; ACC51040.
                                                                                                                                          Query Match
Best Local Similarity
                                                                                                           123 AA;
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Length 123;

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The present invention describes a method of treating cancer associated with prostate stem cell antigen (PSCA) by administering an antibody which selectively binds to PSCA and inhibits the growth of the cancer cells. The PSCA gene is found on human chromosome 8Q24.2. The invention provides the human and murine PSCA protein and coding sequences, which can be used not only in the treatment of, but also in detection and prognosis of
                                                                                                                                                                                                        1 MKAVLIALLMAGIALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prostate stem cell antigen; PSCA; human; mouse; prostate cancer; diagnosis; treatment; chromosome 8q24.2.
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100.0%; Pred. No. 9.4e-78;
ive 0; Mismatches 0;
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1.2e-79;
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                                                                                                                                                                                                                                                                                                61 VISKGCSLNCVDDSQDYYVGKKNITCCDTDLCN 93
                            Query Match 75.6%; Score 93; DB Best Local Similarity 100.0%; Pred. No. 1.2 Matches 93; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human prostate stem cell antigen.
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03-MAY-2000; 2000US-0564329.
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various screening and diagnostic methods, and for gene therapy, vaccine and/or antisense/inhibition applications.
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encoding the peptides, that are useful epitopes of target-associated
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                                                                                                                                                                     Length 123;
                                                                                                                                                                 Query Match 75.6%; Score 93; DB 24; Length 12
Best Local Similarity 100.0%; Pred. No. 1.2e-79;
Matches 93; Conservative 0; Mismatches 0; Indels
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07-NOV-2001; 2001US-337017P.
07-MAR-2002; 2002US-363210P.
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                                                                                                                                                                                                                                                   Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
leukaemia; neuronal disorder; stromal disorder; blastoccelic disorder;
inflammatory disorder; immune disorder; angiogenic disorder;
cytostatic; neuroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thirty five nucleic acids encoding PRO polypeptides, useful for treating benign or malignant tumours, leukaemias and lymphoid malignancies, inflammatory, angiogenic and immunologic disorders
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Stone DM;
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Smith V,
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7e-76;
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i RM, Roy MA,
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100.0%; Pred. No.
                                                                                AAU86131 standard; Protein; 119 AA.
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Pan J, Pitti RM,
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9US-140651P.
9US-14569P.
9US-14522P.
9US-145395P.
9US-149395P.
9US-11689P.
9WO-US20111.
99WO-US20111.
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99US-123972P.
99US-133459P.
99WO-US12252.
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01-DEC-1999; 99WO-US28634.
05-JAN-2000; 2000WO-US00219.
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                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                polypeptide.
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Wood WI;
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N-PSDB; ABK40257.
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Best Local Similarity
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Watanabe CK,
                                                                                                                                                                                                                Human PRO232
                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                 1 LLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLTVISK 60
LLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLTVISK
                                                                                                                                                                                              Zollinger_Ellison syndrome; gastrointestinal ulceration; congenital microvillus atrophy, skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer; Parkinson's disease, Alzheimer's disease; ALS; neuropathy; fibromodulln; dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic; wound healing; tissue repair.
                                                                                                                                                                                      Secreted protein; transmembrane protein; human; enterocolitis;
                                      93
                                                   89
                                                GCSLNCVDDSQDYYVGKKNITCCDTDLCN
                                      GCSLNCVDDSQDYYVGKKNITCCDTDLCN
                                                                                                                                                                 Amino acid sequence of protein PRO232
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                                                                                                        AAY13347 standard; Protein; 114
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97US-0059113.
97US-0059115.
97US-0059117.
97US-0059119.
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97US-0059184.
97US-0059263.
97US-0062125.
97US-0062125.
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97US-0062814.
97US-0062816.
97US-0063045.
97US-0063120.
97US-0063121.
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97US-0063327.
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97US-0063544.
97US-0063549.
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97US-0063564.
97US-0063435.
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97US-0064215.
97US-0063735.
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                                                                                                                                                (first entry)
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29-OCT-1997;
29-OCT-1997;
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Kato S, Kobayashi M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 AA;
                                                                                                                                                                 08-OCT-1997;
                                                                                                                                            05-OCT-1998;
                                                                        Homo sapiens
                                                                                              WO9918203-A2
                                                                                                                     15-APR-1999.
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                                                                                                                                                                                        (PROT-)
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                                                                                                                                                                                                                                                                                                                  AAY13144-403 represent secreted and transmembrane human proteins.

The cDNA sequences are obtained from cDNA libraries, prepared from fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.

The encoded polypeptides have specific uses based on their homology to known polypeptides, e.g. RRO211 and RRO217 can be used for disorders associated with the preservation and maintenance of gastrointestinal mucosa and the repair of acute and chronic mucosal lesions

(e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal ulceration and congenital microvillus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial cancers such as lung squamous cell carcinoma of the vulva and gliomas), potent effects on cell, growth and development, diseases related to growth or survival of nerve cells including Parkinson's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alzheimer's disease, ALS, neuropathies or cancer. PRO265 can be used as for fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used as a target for anti-tunor drugs. PRO563 may be used in the treatment of Usher Syndrome or Atrophia areata; PRO569 can be used as anti-thrombotic agent; PRO287 polypeptides and portions may have therapeutic applications in wound healing and tissue repair; PRO317 can be used for treatments of the Kidney, uterus, endometrium, bloodvessels, or related tissue, e.g. in the heart of genital tract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 MAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIRAVGLLTVISKGCSLN 69
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                                                                                                                                                                                                                                                           New isolated human genes and polypeptides used in, e.g. treatment gastrointestinal ulceration
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                                                                                                                                                                                                      Yuan J;
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                                                                                                                                                                                                      Goddard A, Gurney AL, Pennica D, Wood WI,
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100.0%; Pred. No. 3.4e-71;
ive 0; Mismatches 0;
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97US-00643870.
97US-0064103.
97US-00648103.
97US-0065886.
97US-0065846.
97US-0065846.
97US-0066120.
97US-0066120.
97US-006646.
97US-006646.
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                                                                                                                                                                               (GETH ) GENENTECH INC
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Best Local Similarity
Local 84; Conserva
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N-PSDB; AAX52217.
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18-NOV-1997
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12-NOV-1997
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21-NOV-1997
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03-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              All of the proteins exist in the cell membrane, so are considered to be proteins controlling the proliferation and differentiation of the cells. They may be useful as carcinostatic agents or as antigons for preparing antibodies against the proteins. The CDNAs can be used as probes for gene diagnosis and gene sources for gene therapy, as well as for large-scale expression of the proteins. The HPD1498 (see AAVI333) protein may be associated with signal transduction associated with appotosis, and therefore useful in inhibition of apoptosis. The HPD1962 (see AAVI3943) protein can be used to treat diseases associated with phopshatidylethanolamine N-methyltransferase. The proteins are identified by the presence of a hydrophobic transmembrane region, knowledge of the protein is not required, as in e.g. methods of
Transmembrane protein; human; cell membrane; proliferation; diagnosis; cell differentiation; carcinostatic agent; probe; gene therapy; signal transduction; apoptosis; inhibitor; phopshatidylethanolamine N-methyltransferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence is a human transmembrane protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEGENE INC.
SAGAMI CHEM RES CENT
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Fang YT, Liu C, Drmanac RT; WPI; 2001-457740/49. N-PSDB; ABA09221

cell culture; drug screening; gene therapy; antiinflammatory; antiathmatic; antiatrhritic; haemostatic; antiatreriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antulcer. 03-FEB-2000; 2000US-0496914. 27-APR-2000; 2000US-0560875. 05-FEB-2001; 2001WO-US03800 (HYSE-) HYSEQ INC. WO200157188-A2 Ното варіепв 09-AUG-2001

Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer

Claim 20; Page 291; 1963pp; English.

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, and feel of the invention. Although novel polypeptides, or polypeptides of the invention atthough novel, many of the polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities, including cytokine, cell proliferation or cell differentiation activities, enceptor or ligand activities, or may concern activity; insue growth activity; insue cetivities, or may be included activities, or may activity; activity, tissue growth activity; chemocapitic or chemokinetic activities, haemocapitic or chemokinetic activities, haemocapitic or themokinetic activities, proliferation or metastasis.

Chemololytic activities, activities, proliferation or metastasis.

Chemololytic activities activities, proliferation or metastasis.

Chemololytic activities or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions, e.g., by protein or gene therapy. Such conditions include conditions and ulcers), and abnormal vacuular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promocapies of purns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, because the call growth factor activity may be used in cell culture to aucentic or auchibit or auchibit or auchibit or auchibite the used to augment or auchib autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug techniques. The present sequence represents a novel human can be used to augment or replace cells damaged by illness, immune disease or accidental damage. The polypeptides and nu polypeptide of the invention.

Sequence

ö Gaps .; 0 Length 117; 0; Indels 41.5%; Score 51; DB 22; I 100.0%; Pred. No. 3.9e-40; tive 0; Mismatches 0; 51; Conservative Query Match Best Local Similarity Matches 51; Conserv

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polypoptides (such as this sequence) or PSI16 amplicons are used to detect prostate disease. Antibodies (Abs) against PSI16 are used in assay kits to detect PSI16 antigen or anti-PSI16 Ab, and the Abs are used in assay bSI16-specific Abs in a sample, and for producing Abs after immunishing a subject. Plasmids encoding PSI16 epitopes can also be administered to a subject to obtain Abs. The cDNAs and polypeptides are useful for detecting, diagnosing, staging, monitoring, prognosticating, in vivo subject to diseases and conditions of the predisposition of a subject to diseases and conditions of the predisposition of a concer. The Abs and agonists or inhibitors are useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isolated as expressed sequence tag (EST) clone of the PS116 gene isolated from a human prostate tissue library. The PS116 sequences can be used in the method of the invention for detecting a target PS116 polynucleotide (PN), that comprises: contacting a sample with at least 1 PS116-specific PN or complement; and detecting the target PS116 PN, where the specific PN has at least 50% identity with the PS116 sequences. The PNs, PS116
                                                                                                                                                                                                                                                                                           disease; diagnosis; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a PS116 antigen. The PS116 gene sequences were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New method for detecting diseases of the prostate - comprises use of a PS116 polynucleotide, protein or antibodies, useful for preventing and treating prostate infections and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                              58 VLLALLMAGLALQPGTALLCYSCKAQVSNBDCLQVENCTQLGEQCWTARIR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kratochvil JD;
4 VLLALLMAGLALQPGTALLCYSCKAQVSNEDCLQVENCTQLGEQCWTARIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Friedman PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 RIRAVGLLTVISKGCSLNCVDDSQDYYVGKKNITCCDTDLC 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIRAVGLLTVISKGCSLNCVDDSQDYYVGKKNITCCDTDLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.3%; Score 41; DB 20; I
100.0%; Pred. No. 3.9e-31;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                     Human; expressed sequence tag; EST; prostate dis
detection; therapy; prostate cancer; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Billing-Medel PA, Cohen M, Colpitts TL, Frie
Gordon J, Granados EN, Hodges SC, Klass MR,
Roberts-Rapp L, Russell JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prostate diseases, tumours and metastases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 17; Page 98; 118pp; English.
                                                                                                                                  AAW80958 standard; Protein; 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-US10041.
                                                                                                                                                                                                             16-MAR-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 41; Conserv
                                                                                                                                                                                                                                                     PS116 antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                      WO9851805-A1
                                                                                                                                                                       AAW80958;
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